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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:32:02 ; Search time 31 Seconds
(without alignments)
158.930 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIVTGTWISVKNKQL.....KPSDPWDQAKCYGCKYL 66

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued_Patents_AA:*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	66	2 US-08-511-485-24	Sequence 24, App1
2	386	100.0	66	4 US-09-201-936-24	Sequence 24, App1
3	386	100.0	66	4 US-09-011-356-24	Sequence 24, App1
4	386	100.0	66	4 US-09-201-932-24	Sequence 24, App1
5	386	100.0	496	2 US-08-511-485-10	Sequence 10, App1
6	386	100.0	496	3 US-09-212-971-10	Sequence 10, App1
7	386	100.0	496	3 US-08-800-929A-10	Sequence 10, App1
8	386	100.0	496	3 US-09-617-053A-10	Sequence 10, App1
9	386	100.0	496	4 US-09-201-936-10	Sequence 10, App1
10	386	100.0	496	4 US-09-011-356-10	Sequence 10, App1
11	386	100.0	496	4 US-09-672-717-225	Sequence 225, App1
12	386	100.0	496	4 US-09-201-932-10	Sequence 10, App1
13	386	94.8	66	2 US-08-511-485-25	Sequence 25, App1
14	366	94.8	66	4 US-09-201-936-25	Sequence 25, App1
15	366	94.8	66	4 US-09-011-356-25	Sequence 25, App1
16	366	94.8	66	4 US-09-201-932-25	Sequence 25, App1
17	366	94.8	236	3 US-09-239-867-4	Sequence 4, App1
18	366	94.8	236	4 US-10-024-433-4	Sequence 4, App1
19	366	94.8	497	2 US-08-511-485-4	Sequence 4, App1
20	366	94.8	497	3 US-09-212-971-4	Sequence 4, App1
21	366	94.8	497	3 US-08-800-929A-4	Sequence 4, App1
22	366	94.8	497	3 US-09-617-053A-4	Sequence 4, App1
23	366	94.8	497	4 US-08-657-759-2	Sequence 2, App1
24	366	94.8	497	4 US-09-201-936-4	Sequence 4, App1
25	366	94.8	497	4 US-09-011-356-4	Sequence 4, App1
26	366	94.8	497	4 US-09-672-717-219	Sequence 219, App1
27	366	94.8	497	4 US-09-201-932-4	Sequence 4, App1

28	366	94.8	497	4 US-09-949-016-6032	Sequence 6032, App1
29	334	86.5	236	3 US-09-121-979-4	Sequence 4, App1
30	334	86.5	236	3 US-09-332-319-4	Sequence 4, App1
31	334	86.5	236	3 US-09-239-867-2	Sequence 2, App1
32	334	86.5	236	4 US-10-024-433-2	Sequence 2, App1
33	279	72.3	53	4 US-08-657-759-19	Sequence 19, App1
34	233	60.4	50	3 US-08-975-080-28	Sequence 28, App1
35	233	60.4	50	3 US-08-975-080-29	Sequence 28, App1
36	233	60.4	50	3 US-08-975-080-32	Sequence 28, App1
37	233	60.4	50	4 US-10-138-618-28	Sequence 28, App1
38	233	60.4	50	4 US-10-138-618-29	Sequence 29, App1
39	233	60.4	50	4 US-10-138-618-32	Sequence 32, App1
40	198	51.3	68	2 US-08-511-485-26	Sequence 26, App1
41	198	51.3	68	4 US-09-201-936-26	Sequence 26, App1
42	198	51.3	68	4 US-09-011-356-26	Sequence 26, App1
43	198	51.3	68	4 US-09-201-932-26	Sequence 26, App1
44	198	51.3	442	4 US-09-579-6928-58	Sequence 58, App1
45	198	51.3	604	2 US-08-511-485-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-08-511-485-24
Sequence 24, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULAR TYPE: protein
US-08-511-485-24
Query Match 100.0%; Score 386; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4,1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIVTGTWISVKNKQLAGFYALBGDKYKCFHCGGGLTDWKPSPDPDQAKCY 60

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Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
QY 61 PGCKYL 66
   |||||
   61 PGCKYL 66

Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
QY 61 PGCKYL 66
   |||||
   61 PGCKYL 66

RESULT 2
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
QY 61 PGCKYL 66
   |||||
   61 PGCKYL 66

Db 61 PGCKYL 66
   |||||
   61 PGCKYL 66

RESULT 3
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
QY 61 PGCKYL 66
   |||||
   61 PGCKYL 66

Db 61 PGCKYL 66
   |||||
   61 PGCKYL 66

RESULT 4
US-09-201-932-24
; Sequence 24, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
Db 1 YEARIVTGTWTVSYVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHAACY 60
QY 61 PGCKYL 66
   |||||
   61 PGCKYL 66

Db 61 PGCKYL 66
   |||||
   61 PGCKYL 66

RESULT 5
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/08/511,485
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-10

Query Match 100.0%; Score 386; DB 2; Length 496;

Best Local Similarity 100.0%; Pred. No. 4.7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIVTFTWISVVKKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 264 YEARIVTFTWISVVKKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
US-09-212-971-10
Sequence 10, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT

ORGANISM: Mus musculus
US-09-212-971-10

Query Match 100.0%; Score 386; DB 3; Length 496;

Best Local Similarity 100.0%; Pred. No. 4.7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIVTFTWISVVKKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 264 YEARIVTFTWISVVKKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
US-08-800-929A-10

Sequence 10, Application US/08800929A
Patent No. 6133437

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045
TELEX:

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-800-929A-10

Query Match 100.0%; Score 386; DB 3; Length 496;

Best Local Similarity 100.0%; Pred. No. 4.7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YEARIVTFGFWIYSVNKEQLARAGFYALGEGDKVNCFCFGGLTDMKSESDPMQHKCY	60
Db	264	YEARIVTFGFWIYSVNKEQLARAGFYALGEGDKVNCFCFGGLTDMKSESDPMQHKCY	322
Qy	61	PGCKYL	66
Db	324	PGCKYL	329

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RESULT 8
US-09-617-053A-10
: Sequence 10: Application US/09617053A
: Patent No. 6300492
: GENERAL INFORMATION:
: APPLICANT: Korneluz, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Charlene
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009003
: CURRENT APPLICATION NUMBER: US/09/617,053A
: CURRENT FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US/08/800,929
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 496
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-617-053A-10

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[illegible]

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RESULT 9
US-09-201-936-10
Sequence 10. Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneiluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Irlston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FaalSeq for Windows Version 3.0

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; SEQ ID NO 10
; LENGTH: 496
; TYPE: prt
; ORGANISM: Mus musculus
US-09-201-936-10

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Query Match	100.0%;	Score 386;	DB 4;	Length 496;
Best Local Similarity	100.0%;	Pred. No. 4.7e-42;		
Matches 66;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	YEARITPCGMWISVVKEOIAPAGFYALAGEBDKVCFCFGGGLTDMKRSBDPMQNAKCY	60
D6	264	YEARITPCGMWISVVKEOIAPAGFYALAGEBDKVCFCFGGGLTDMKRSBDPMQNAKCY	323
QY	61	PGCKYTL	66
D6	324	PGCKYTL	329

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RESULT 10
US-09-011-356-10
; Sequence 10, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneljuk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Hinton, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 078921/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-011-356-10

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Query Match	100.0%	Score 386;	DB 4;	Length 496;
Best Local Similarity	100.0%	Pred. No. 4.7e-42;		
Matches 66; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	YEARIITPTFTWYISVNKQQLARAGYALGEBDKYKCFPGGGGLTDMKPSSEDPMDQNAKCY	60
Db	264	YEARIITPTFTWYISVNKQQLARAGYALGEBDKYKCFPGGGGLTDMKPSSEDPMDQNAKCY	323
Qy	61	PGCKTL 66	
Db	324	PGCKTL 329	

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RESULT 11
US-09-672-717-225
? Sequence 225, Application US/09672717
? Patent No. 6673917
? GENERAL INFORMATION:
? APPLICANT: Korneluk, Robert G.
? APPLICANT: Lacasse, Eric
? APPLICANT: Baird, Stephen
? APPLICANT: Holcik, Martin
? APPLICANT: Young, Sean
? TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
? TITLE OF INVENTION: Theretol
? FILE REFERENCE: 07891/025001

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; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-672-717-225

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Query Match      100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 4,7e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 60
Db      264 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 323
Qy      61 PGCKYL 66
Db      324 PGCKYL 329

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RESULT 12
US-09-201-932-10
; Sequence 10, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-10

```

```

Query Match      100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 4,7e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 60
Db      264 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 323
Qy      61 PGCKYL 66
Db      324 PGCKYL 329

```

```

RESULT 13
US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.

```

```

; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acid
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-25

```

```

Query Match      94.8%; Score 366; DB 2; Length 66;
Best Local Similarity 95.5%; Pred. No. 1,7e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

Qy      1 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 60
Db      1 YEARIVFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMDOHAKCY 60
Qy      61 PGCKYL 66
Db      61 PGCKYL 66

```

```

RESULT 14
US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45

```

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match
Best Local Similarity 94.8%; Score 366; DB 4; Length 66;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 15
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-011-356-25

Query Match

Best Local Similarity 94.8%; Score 366; DB 4; Length 66;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 16
US-09-201-932-25
; Sequence 25, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003004

CURRENT APPLICATION NUMBER: US/09/201,932A
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-932-25

Query Match
Best Local Similarity 94.8%; Score 366; DB 4; Length 66;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 17
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:

APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-239-867-4

Query Match

Best Local Similarity 94.8%; Score 366; DB 3; Length 236;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 4 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 63

QY 61 PGCKYL 66
|||
Db 64 PGCKYL 69

RESULT 18
US-10-024-433-4
; Sequence 4, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:

APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
FILE REFERENCE: MALE FERTILITY

FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/10/024,433
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/239,867
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-433-4

Query Match 94.8%; Score 366; DB 4; Length 236;
Best Local Similarity 95.5%; Pred. No. 7.9e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 60
DB 4 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 19
US-08-511-485-4
Sequence 4, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-4

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 60
DB 265 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 20
US-09-212-971-4
Sequence 4, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 60
DB 265 YEARIPTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMQHAACY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 21
US-08-800-929A-4
Sequence 4, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPs AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,923A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-923A-4

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 22
US-09-617-053A-4
Sequence 4, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-4

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 23
US-08-657-759-2
Sequence 2, Application US/08657759
Patent No. 6511828
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Duckett, Colin S.
TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,759
FILING DATE: 31-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-2

Query Match 94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 24
US-09-201-936-4
Sequence 4, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:

```

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1996/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 25
US-09-011-356-4
; Sequence 4, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/1996/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324

```

```

QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 26
US-09-672-717-219
; Sequence 219, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; EARLIER FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-717-219

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```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 27
US-09-201-932-4
; Sequence 4, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1996/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;

```

Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
Db 265 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKMY 324

Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 28

US-09-949-016-6032
; Sequence 6032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6032
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6032

Query Match 94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
Db 265 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKMY 324

Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 29

US-09-121-979-4
; Sequence 4, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-979-4

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
Db 4 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLANWKPKEDPMEQHAKEY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 30

US-09-332-319-4
; Sequence 4, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-332-319-4

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
Db 4 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLANWKPKEDPMEQHAKEY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 31

US-09-239-867-2
; Sequence 2, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-2

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
Db 4 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLANWKPKEDPMEQHAKEY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 32

US-10-024-433-2
; Sequence 2, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-2

Query Match 86.5%; Score 334; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYVFTWISVKNKQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKY 60
Db 4 YEARIYVFTWISVKNKQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 33

US-08-657-759-19
; Sequence 19, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-May-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-19

Query Match 72.3%; Score 279; DB 4; Length 53;
Best Local Similarity 95.9%; Pred. No. 3.1e-29;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 18 EQARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 66
Db 1 EQARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 49

RESULT 34

US-08-975-080-28
; Sequence 28, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7176
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-080-28

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 66
Db 1 ALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 40

RESULT 35
US-08-975-080-29
; Sequence 29, Application US/08975080
; Patent No. 6245523

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-29

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCFGGGLTDMKPSDEPDWDHAKCYPGCKYL 66
DB 1 ALGEGDKVCKFCFGGGLTDMKPSDEPDWDHAKCYPGCKYL 40

RESULT 36
US-08-975-080-32
Sequence 32, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7000
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-32

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCFGGGLTDMKPSDEPDWDHAKCYPGCKYL 66
DB 1 ALGEGDKVCKFCFGGGLTDMKPSDEPDWDHAKCYPGCKYL 40

RESULT 37
US-10-138-618-28
Sequence 28, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 40

RESULT 38
US-10-138-618-29
Sequence 29, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 40

RESULT 39
US-10-138-618-32
Sequence 32, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVKCFHCGGGLTDWKPSEDPWDQAKCYPGCKYL 40

RESULT 40
US-08-511-485-26
Sequence 26, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-26

Query Match 51.3%; Score 198; DB 2; Length 68;
 Best Local Similarity 55.9%; Pred. No. 1.7e-18;
 Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY	1	YEARIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQAK	58
Db	1	HAARFKTFPMWSSVLVNPQLASAGFYVYGNSDVVKCFCCDGLRCMESGDDPMTQAK	60
QY	59	CYPGCKYL	66
Db	61	WFPRCXYL	68

Search completed: June 15, 2005, 17:53:09
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:18:26 ; Search time 115 seconds
(without alignments)
221.967 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYVFTGWTIVSNKREQL.....KPSHPDWDHAKCYGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp19806:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	386	100.0	496	2	AAW19584 Mouse apo
2	386	100.0	496	2	AAW69297 Murine XI
3	386	100.0	496	5	ABG65666 Mouse inh
4	372	96.4	66	7	ADB61828 Mouse inh
5	372	96.4	496	6	ABP72157 Mouse inh
6	366	94.8	66	7	ADB61827 Rat inh
7	366	94.8	66	7	ADB61810 Human inh
8	366	94.8	110	8	ADP90805 Human XIA
9	366	94.8	236	5	ABG32418 X-linked
10	366	94.8	278	5	AAO20511 Protein o
11	366	94.8	497	2	AAW19581 Human apo
12	366	94.8	497	2	AAW69294 Human XIA
13	366	94.8	497	3	AAV59451 Human XIA
14	366	94.8	497	3	AAV99985 Human X-1
15	366	94.8	497	5	ABG65663 Human inh
16	366	94.8	497	7	ADB80961 RING-SH c
17	366	94.8	497	7	AD139804 Human inh
18	366	94.8	497	8	ADH74639 Human XIA
19	366	94.8	497	8	ADL70166 Human X c
20	366	94.8	497	8	ADP23982 PRO polyP
21	357	92.5	496	7	AAW19745 Human inh
22	357	92.5	66	7	ADB61820 Human inh
23	334	86.5	236	3	AAV81440 Human TIA
24	334	86.5	236	4	AAE00365 Human TAP
25	334	86.5	236	5	AAU75066 Human tes

26	334	86.5	236	5	ABG32417	ABG32417 Inhibitor
27	334	86.5	464	5	AAU75747	AAU75747 Human inh
28	328	85.0	236	4	AAE00366	AAE00366 Chimpanzee
29	326.5	84.6	87	8	ADR44576	ADR44576 X-IAP BIR
30	325	84.2	66	7	ADB61831	ADB61831 Gorilla i
31	325	84.2	236	4	AAE00367	AAE00367 Gorilla i
32	306	79.3	57	7	ADB61832	ADB61832 Unidentif
33	279	72.3	53	7	AD139821	AD139821 Human NAI
34	279	72.3	66	7	ADB61829	ADB61829 Chicken i
35	260	67.4	151	5	ADK34975	ADK34975 Novel hum
36	258	66.8	52	7	ADB61830	ADB61830 Bovine in
37	212	54.9	68	7	ADB61833	ADB61833 Zebra fib
38	198	51.3	68	7	ADB61813	ADB61813 Human inh
39	198	51.3	442	8	ADO26592	ADO26592 Human API
40	198	51.3	557	6	ABP72159	ABP72159 Inhibitor
41	198	51.3	604	2	AAW19582	AAW19582 Human apo
42	198	51.3	604	2	AAW19747	AAW19747 Human inh
43	198	51.3	604	2	AAW13546	AAW13546 Human C-I
44	198	51.3	604	2	AAW69295	AAW69295 Human HIA
45	198	51.3	604	2	AAV52703	AAV52703 Human cel

ALIGNMENTS

RESULT 1	AAW19584	standard; protein; 496 AA.
ID	AAW19584	standard; protein; 496 AA.
XX	AAW19584;	
XX	AC	
XX	DT	02-SEP-1997 (first entry)
XX	DE	Mouse apoptosis inhibitor M-XIAP.
XX	KM	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW	HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischemia;	
KW	myocardial infarction; stroke; reperfusion injury;	
KW	toxin-induced liver disease; gene therapy; diagnosis.	
XX	OS	Mus sp.
XX	FH	Key
FT	Domain	Location/Qualifiers
FT	Domain	26..93
FT	Domain	/label= BIR-1
FT	Domain	163..230
FT	Domain	/label= BIR-2
FT	Domain	264..329
FT	Domain	/label= BIR-3
FT	Domain	438..483
FT	Domain	/label= Ring_zinc_finger
XX	PN	W09706255-A2.
XX	PD	20-FEB-1997.
XX	XX	
XX	PE	05-AUG-1996; 96WC-IB001022.
XX	PR	04-AUG-1995; 95US-00511485.
XX	PR	22-DEC-1995; 95US-00576956.
XX	PA	(UYOT-) UNIV OTTAWA.
XX	PI	korneljuk RG, Mackenzie AE, Baird S, Liston P;
XX	XX	WPI; 1997-154262/14.
XX	DR	N-PSDB; AAT70839.
XX	XX	
PT	PT	Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT	PT	suppress apoptosis in e.g. HIV or AIDS patients, and for detection of
PT	PT	susceptibility to apoptotic disease.
XX	PS	Claim 27; Page 79-80; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
 CC was deduced from the m-xiap gene (AA170839) isolated from a mouse embryo
 CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
 CC vitro or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 CC
 SQ Sequence 496 AA;
 Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYVKNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFGTWIYVKNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMDOHAKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329
 RESULT 2
 AAW69297
 ID AAW69297 standard; protein; 496 AA.
 AC AAW69297;
 XX 13-NOV-1998 (first entry)
 DT 13-NOV-1998 (first entry)
 XX
 DE Murine XIAP protein.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KM proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
 XX
 OS Mus sp.
 XX
 PN WO9835693-A2.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98MO-IB000781.
 XX
 PR 13-FEB-1997; 97US-00800929.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX
 DR WPI, 1998-467164/40.
 DR N-PSDB; AAV55041.
 XX
 XX
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX
 XX
 PS Disclosure; Fig 4; 147p; English.
 XX
 CC This sequence is the murine XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver neoplasmyx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 CC
 SQ Sequence 496 AA;
 Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYVKNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFGTWIYVKNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMDOHAKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329
 RESULT 3
 ABG65666
 ID ABG65666 standard; protein; 496 AA.
 AC ABG65666;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Mouse inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; antisense; inhibitor of apoptosis; HIAP1, HIAP2, XIAP; cytosolic;
 KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KM embryonic development; viral pathogenesis; autoimmune disorder;
 KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KM herpes virus infection; pox virus infection; adenovirus infection;
 KM proliferative disease.
 XX
 OS Mus sp.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001MO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (AECE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI, 2002-479562/51.
 DR N-PSDB; ABX93872.
 XX
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX
 XX
 PS Example 12; Fig 4; 135p; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 386; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 2e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIYFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMQHAQCY 60
DB 264 YEARIYFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMQHAQCY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 4
ADB61828
ID ADB61828 standard; protein; 66 AA.
AC ADB61828;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM H1AP1; GIAP2; H1AP2; GIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytostatic; neoplasm; leukemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms' tumour; BIR 3 domain; mouse; murine.
XX
OS Mus sp.
PN MO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002MO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
PR 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Boudreaux A, Korneluk RG, La Casse E, Liston P;
XX
DR WPI; 2003-513532/48.
XX
PT Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1
CC (GIAP2) and H1AP2 (GIAP1) all possess three BIR domains and a caspase
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.
XX
SQ Sequence 66 AA;
Query Match 96.4%; Score 372; DB 7; Length 66;
Best Local Similarity 97.0%; Pred. No. 1.e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMQHAQCY 60
DB 1 YEARIYFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMQHAQCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66
RESULT 5
ABP72157
ID ABP72157 standard; protein; 496 AA.
AC ABP72157;
XX
DT 22-APR-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis protein MIAP3.
XX
XX Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukemia;
KM lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
XX
OS Mus sp.
PN MO2003004606-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002MO-US021002.
XX
PR 03-JUL-2001; 2001US-00698158.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Troy CM, Shelanski ML;
XX
DR WPI; 2003-210351/20.
XX
DR N-PSDB; ABZ58102.
XX
PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
PT treating cancer, neurodegenerative disorder or cardiomyopathy.
XX
PS Disclosure; Fig 15A; 124pp; English.
XX
CC The present sequence is the protein sequence of murine inhibitor of
CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as

CC	an antisense oligonucleotide, which specifically hybridises to a nucleic acid encoding an inhibitor of apoptosis protein, especially XIAP1, XIAP2, XIAP3, XIAP1, XIAP2 and XIAP. A claimed method for inducing a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to treat acute lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all claimed)
SQ	Sequence 496 AA;
Query Match	96.4%; Score 372; DB 6; Length 496;
Best Local Similarity	97.0%; Pred. No. 1.1e-37;
Matches 64; Conservative	0; Mismatches 2; Indels 0; Gaps 0
DY	1 YEARIVTPECTWTVSYNKKEDQLARGFALGEGDKVCKFCFGGGGLTDWKPSDDPDQAKCY 60
DB	264 YEARIVTFTGTWTSSVNKEQLARAGFYALGEGDKVCFCFGGGGLTDWKPSDDPDQAKCY 323
DY	61 PGCKTL 66 324 PGCKTL 329
RESULT 6	
ADEB1827	
ID	ADEB1827 standard; protein; 66 AA.
XX	ADEB1827;
AC	
DT	04-DEC-2003 (first entry)
XX	
DE	Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX	
KM	baculovirus inhibitor of apoptosis repeat domain; BIR domain; apoptosis pathway; embryonic development; viral pathogenesis; cancer; autoimmune disorder; neurodegenerative disease; apoptotic response; systemic lupus erythematosus; multiple sclerosis; viral infection; herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP; XIAP1, XIAP2, XIAP3, XIAP4, XIAP5, XIAP6, XIAP7, XIAP8, XIAP9, caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma; cervical cancer; uterine cancer; testicular cancer; small cell lung carcinoma; uterine cancer; renal cell carcinoma; Wilms' tumor; BIR 3 domain; rat.
KW	
KV	
WM	
OS	Rattus sp.
XX	
PN	WO2003040172-A2.
XX	
PD	15-MAY-2003.
XX	
PF	12-NOV-2002; 2002MO-CA001738.
XX	
PR	09-NOV-2001; 2001US-0332300P.
PR	08-APR-2002; 2002US-0370934P.
XX	
PA	(AEGE-) AEGERA THERAPEUTICS INC.
XX	
P1	Boudreaux A, Korneluk RG, La Casse E, Liston P,
DR	WPI; 2003-513532/48.
XX	
PT	Polypeptide capable of forming a complex with a polypeptide comprising a baculovirus inhibitor of apoptosis repeat domain useful for treating cancer and other neoplasms.
PT	
XX	
PS	Disclosure; Fig 1B; 53pp; English.
CC	This invention relates to a substantially pure polypeptide having a length of less than 100 amino acids and capable of forming a complex with a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

	BIRD	(BIR) domain. The apoptosis pathway is known to play a critical role in embryonic development, viral pathogenesis, cancer, autoimmune disorders and neurodegenerative diseases. The failure of the apoptotic response has been implicated in the development of cancer, autoimmune disorders (for example systemic lupus erythematosus and multiple sclerosis) and viral infections (including herpes virus, poxvirus and adenovirus). The inhibitors of apoptosis (IAPs) are a family of proteins possessing one or more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAIPI (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and -9 which are proteases involved in the initiation of apoptosis. Compounds which inhibit the activity of IAPs may therefore have cytostatic activity through the enhancement of apoptosis. The polypeptides of the invention are candidate peptide ligands for binding to the BIR domain of IAPs. They may be useful for the treatment of cancer and other neoplasms, such as leukaemia; colon carcinoma, cervical cancer, uterine cancer, testicular cancer, small cell lung carcinoma, urologic cancer, renal cell carcinoma and Wilms' tumour, and for enhancing apoptosis. The present sequence is that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain which was used to demonstrate homology to human IAP protein BIR domains to which the peptides of the invention are targeted to bind.
SQ	Sequence 66 AA;	
	Query Match 94.8%; Score 366; DB ?; Length 66; Best Local Similarity 93.9%; Pident.No. 6.le-38; Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
OY	1 YEATVTFGWTIVSYVNKEQLARAGFYALGEDSDKRCFCFGGLTDMKSSEDPMDHACY :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 1 YDAITVFPGTWLTSYNKEQLARAGFYALGEDSKVKCFHCGGSLTDWKPSPDEQHAKMY 60	
OY	61 PGCKYL 66 Db 61 PGCKTL 66	
ID	RESULT 7 ADB61810 standard; protein; 66 AA. XX ADB61810; AC XX DT 04-DEC-2003 (first entry) XX DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.	
KX	baculovirus inhibitor of apoptosis repeat domain; BIR domain; KW apoptosis pathway; embryonic development; viral pathogenesis; cancer; KV autoimmune disorder; neurodegenerative disease; apoptotic response; KM systematic lupus erythematosus; multiple sclerosis; viral infection; KK herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP, KI HAIPI; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7; KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma; KV cervical cancer; uterine cancer; testicular cancer; KW small cell lung carcinoma; uterine cancer; renal cell carcinoma; WM Wilms' tumor; human; BIR 3 domain. OS Homo sapiens. XX PN WO2003040172-A2. PD XX 15-MAY-2003. PP XX 12-NOV-2002; 2002WO-CIA001738. PF 09-NOV-2001; 2001US-033230P. PR 08-APR-2002; 2002US-0370934P. XX PA (AEGE-) AEGERA THERAPEUTICS INC. XI BI Boudreaux A., Korneluk RG, La Casse E., Liston P,	

DR WPI; 2003-513532/48.
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1A; 53pp; English.
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HAPI2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC against which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 66 AA;
 Query Match 94.8%; Score 366; DB 7; Length 66;
 Best Local Similarity 95.5%; Pred. No. 6.1e-38;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYTFGTWIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 60
 DB 1 YEARIYTFGTWIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 60
 QY 61 PGCKYL 66
 DB 61 PGCKYL 66
 RESULT 8
 ADP90805
 ID ADP90805 standard; peptide; 110 AA.
 XX
 AC ADP90805;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human XIAP protein BIR-3 domain.
 XX
 KW protein labelling; peptide labelling;
 KW irreversible affinity tagging residue;
 KW reversible affinity tagging residue; high throughput screening assay;
 KW pharmaceutical agent; human; XIAP; BIR-3.
 XX
 OS Homo sapiens.
 XX
 PN WO2004051270-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 04-DEC-2003; 2003WO-EP013715.
 XX
 PR 05-DEC-2002; 2002GB-00028429.
 XX
 PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.
 XX
 PI Auer M, Melener N, Seifert J;
 XX
 DR WPI; 2004-480677/45.
 XX
 XX Providing labeled target protein or target peptide by contacting chemical
 PT compound with affinity support, removing impurities in reaction mixture
 PT surrounding affinity support, cleaving or eluting chemical molecule from
 PT affinity support.
 XX
 PS Example 6; Page 46; 81pp; English.
 XX
 PS The invention comprises a method for providing a labelled target
 CC protein/peptide. The method involves contacting a chemical compound with
 CC affinity support, removing impurities in the reaction mixture surrounding
 CC the affinity support to which the chemical molecule is bound, and
 CC cleaving or eluting the molecule from the affinity support to obtain
 CC irreversible or reversible affinity tagging residue, labelled target
 CC protein or labelled peptide. The method of the invention is useful for
 CC labelling a target protein/peptide or high throughput screening assay.
 CC The method of the invention is useful for identifying agents that
 CC modulate the activity or characteristics of a target protein/peptide -
 CC such agents are useful as pharmaceuticals. The present amino acid
 CC sequence represents the BIR-3 domain from the human XIAP protein which
 CC was used in an example of the invention.
 XX
 SQ Sequence 110 AA;
 Query Match 94.8%; Score 366; DB 8; Length 110;
 Best Local Similarity 95.5%; Pred. No. 1.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYTFGTWIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 60
 DB 17 YEARIYTFGTWIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 76
 QY 61 PGCKYL 66
 DB 77 PGCKYL 82
 RESULT 9
 ABG32418
 ID ABG32418 standard; protein; 236 AA.
 XX
 AC ABG32418;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE X-linked inhibitor of apoptosis protein, XIAP.
 XX
 KW Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
 KW fertility; testicular cancer; male infertility; male birth control;
 KW X-linked inhibitor of apoptosis protein; XIAP.
 XX
 OS Mammalia.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Encoded by nnn; start codon is illegible in
 FT specification"
 XX
 PN US2002086409-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 18-DEC-2001; 2001US-00024433.
 XX
 PR 29-JAN-1998; 98US-0073001P.
 PR 29-JAN-1999; 99US-00239867.
 XX
 PA (KORN/) KORNELUK R G.

PA (LAGA/) LAGAGE M.
XX
XX Kornejux RG, Lagace M;
XX
XX WPI: 2002-642245/69.
XX N-PSDB; ABS52803.
XX
PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins
PT that is expressed in testes useful for modulating apoptosis in cells,
PT particular cells involved in male fertility.
XX
XX Example 3; Fig 4B; 24pp; English.
XX
CC A substantially pure TIAP polypeptide (1), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (1) is
CC useful for identifying a compound that modulates TIAP biological activity
CC (1) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (1) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. TIAP may be manipulated for use as a male
CC birth control. TIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the amino
CC acid sequence of X-linked inhibitor of apoptosis protein, XIAP
XX
SQ Sequence 236 AA;
Query Match 94.8%; Score 366; DB 5; Length 236;
Best Local Similarity 95.5%; Pred. No. 2.7e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSBPDMDHAKCY 60
DB 4 YEARIYFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSBPDMDHAKWY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69
RESULT 10
AAO20511
ID AAO20511 standard; protein; 278 AA.
XX
XX AAO20511;
XX
XX 27-JUN-2002 (first entry)
XX
XX Protein of APP related human homologue hCP35211.
XX
XX Neuroprotective; neurotrophic; transgenic fly; Alzheimer's disease; Abeta;
XX amyloid precursor protein; tissue-specific expression control; human APP;
XX APP pathway modulator; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200226620-A2.
XX
XX 04-APR-2002.
XX
XX 01-OCT-2001; 2001WO-EP011345.
XX
XX 29-SEP-2000; 2000US-023693P.
XX
XX 14-JUN-2001; 2001US-0298309P.
XX
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
XX
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konosolaki M,
XX Reinhardt MMH, Zisman S,
XX
XX WPI: 2002-315796/35.
XX
XX N-PSDB; AAK99405.
XX

XX
XX New transgenic fly, containing DNA encoding an Abeta portion of human
XX APP, useful for identifying agents which modulate the APP pathway and
XX PT which can be used to treat Alzheimer's disease.
XX
XX Example 4; Page 112; 129pp; English.
XX
XX The invention relates to a transgenic fly whose genome comprises DNA
XX encoding a polypeptide having the Abeta portion of human amyloid
XX precursor protein (APP), fused to a signal sequence. The DNA sequence
XX encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
XX the specification. The DNA sequence is operably linked to a tissue-
XX specific expression control sequence. Expression of the sequence gives
XX the fly an altered phenotype. The purpose of the invention is for
XX identifying agents that inhibit or promote the expression and/or function
XX of genes or encoded polypeptides which modify the APP pathway. The agent
XX is a compound, triple helix DNA, antisense oligonucleotide, double
XX stranded RNA molecule, ribozyme, or particularly an antibody. It is used
XX to treat conditions such as Alzheimer's disease. The agent can be used as
XX an APP pathway modulator or in gene therapy. This sequence represents the
XX protein of the APP related human homologue hCP35211
XX
SQ Sequence 278 AA;
Query Match 94.8%; Score 366; DB 5; Length 278;
Best Local Similarity 95.5%; Pred. No. 3.3e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSBPDMDHAKCY 60
DB 46 YEARIYFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSBPDMDHAKWY 105
QY 61 PGCKYL 66
DB 106 PGCKYL 111
RESULT 11
AAW19581
ID AAW19581 standard; protein; 497 AA.
XX
XX AAW19581;
XX
XX 02-SEP-1997 (first entry)
XX
XX Human apoptosis inhibitor XIAP.
XX
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
XX AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
XX myocardial infarction; stroke; reperfusion injury;
XX toxin-induced liver disease; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT Domain 26..93
XX FT Domain /label= BIR-1
XX FT Domain 163..230
XX FT Domain /label= BIR-2
XX FT Domain 265..330
XX FT Domain /label= BIR-3
XX FT Domain 439..484
XX FT Domain /label= Ring_zinc_finger
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB001022.
XX
XX 04-AUG-1995; 95US-00511485.
XX
XX 22-DEC-1995; 95US-00576956.
XX

PA (UYOT-) UNIV OTTAWA.
 XX Korneljuk RG, Mackenzie AB, Baird S, Liston P;
 XX WPI: 1997-154262/14.
 DR N-PSDB; AAT70836.
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.
 XX Claim 27; Page 68-70; 219pp; English.
 XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 CC
 SQ Sequence 497 AA;
 XX
 Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYFTGWTIYVSKQLARAGFYALGSDGVKCFHCGGLTDMKPSDPMQHAQCY 60
 Db 265 YEARIYFTGWTIYVSKQLARAGFYALGSDGVKCFHCGGLTDMKPSDPMQHAQCY 324
 QY 61 PGCKYTL 66
 Db 325 PGCKYTL 330
 Db
 RESULT 12
 AAW69294 ID AAW69294 standard; protein: 497 AA.
 XX
 AC AAW69294;
 XX
 DT 13-NOV-1998 (first entry)
 XX
 DE Human XIAP protein.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KM proliferative disease; IAP; therapy; cancer; human; XIAP protein.
 XX
 OS Homo sapiens.
 OS
 PN WO9835693-A2.
 PN
 PD 20-AUG-1998.
 PD
 PF 13-FEB-1998; 98WO-IB000781.
 PF
 PR 13-FEB-1997; 97US-00800929.
 PR
 XX (UYOT-) UNIV OTTAWA.
 PA
 PI Korneljuk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX WPI: 1998-467164/40.
 DR N-PSDB; AAV55038.
 DR
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP

PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX
 XX Disclosure; Fig 1; 147pp; English.
 XX
 CC This sequence is the human XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 CC
 SQ Sequence 497 AA;
 XX
 Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYFTGWTIYVSKQLARAGFYALGSDGVKCFHCGGLTDMKPSDPMQHAQCY 60
 Db 265 YEARIYFTGWTIYVSKQLARAGFYALGSDGVKCFHCGGLTDMKPSDPMQHAQCY 324
 QY 61 PGCKYTL 66
 Db 325 PGCKYTL 330
 Db
 RESULT 13
 AAY59451 ID AAY59451 standard; protein: 497 AA.
 XX
 AC AAY59451;
 XX
 DT 24-MAR-2000 (first entry)
 XX
 DE Human XIAP protein sequence.
 XX
 KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta.
 XX
 OS Homo sapiens.
 OS
 PN JP1326328-A.
 PN
 PD 26-NOV-1999.
 PD
 PF 13-MAY-1998; 98JP-00130378.
 PF
 PR 13-MAY-1998; 98JP-00130378.
 PR
 XX (MATS/) MATSUMOTO K.
 PA
 DR WPI: 2000-078337/07.
 DR
 DR N-PSDB; AA248862.
 DR
 XX Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 PT
 PS Claim 3; Page 28-30; 43pp; Japanese.
 XX
 CC This sequence represents the human XIAP protein. The invention relates to
 CC a method for screening a substance inhibiting the formation of a complex

CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
 CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
 CC protein 1 (TAB1) and a substance to be tested are contacted with each
 CC other and then the presence or formation of a complex between XIAP and
 CC TAB1 is detected. The substance can be used as a drug for extracellular
 CC matrix protein production enhancement, cell growth inhibition, monocyte
 CC migration, physiologically active substance induction, immunosuppression,
 CC and beta-amyloid protein deposition. A substance inhibiting the formation
 CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
 CC (transforming growth factor-beta) type I and/or type II receptor is
 CC useful as a drug

CC
 XX
 SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;

Best Local Similarity 95.5%; Pred. No. 6,4e-37;

Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Dy 1 YEARIYFGTWIYVSNKEQLARAGFYALGEGDKYKCHCGGLTDMKPSDPMDOHAKCY 60

Db 265 YEARIYFGTWIYVSNKEQLARAGFYALGEGDKYKCHCGGLTDMKPSDPMDOHAKMY 324

Dy 61 PGCKYL 66

Db 325 PGCKYL 330

Db

RESULT 14
 AAY99985

ID AAY99985 standard; protein; 497 AA.

XX

DT 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis.

XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
 XX antiinflammatory; cytostatic; tumour.

XX Homo sapiens.

PN US6087173-A.

PD 11-JUL-2000.

PF 09-SEP-1999; 99US-00392580.

PR 09-SEP-1999; 99US-00392580.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowser LM, Ackermann EJ;

XX WPI: 2000-498201/44.

DR N-PSDB; AAA64901.

XX Antisense compound useful for research reagents, diagnostics, prophylaxis
 XX and for treating disorders associated with X-linked inhibitor of
 XX apoptosis, modulates expression of X-linked inhibitor of apoptosis.

PS Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 XX inhibit expression of the human X-linked inhibitor of apoptosis (the
 XX present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
 XX more effective inhibitors than unmodified oligonucleotides. The
 XX oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 XX expression in cells and tissues in vitro. The oligonucleotides are also
 XX useful for treating animals or humans, prone to a disease associated with
 XX X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 XX prophylactically to prevent infection, inflammation or tumour formation

SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;

Best Local Similarity 95.5%; Pred. No. 6,4e-37;

Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Dy 1 YEARIYFGTWIYVSNKEQLARAGFYALGEGDKYKCHCGGLTDMKPSDPMDOHAKCY 60

Db 265 YEARIYFGTWIYVSNKEQLARAGFYALGEGDKYKCHCGGLTDMKPSDPMDOHAKMY 324

Dy 61 PGCKYL 66

Db 325 PGCKYL 330

Db

RESULT 15
 ABG65663

ID ABG65663 standard; protein; 497 AA.

XX ABC65663;

DT 26-AUG-2002 (first entry)

XX Human inhibitor of apoptosis, XIAP.

XX Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 XX cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 XX embryonic development; viral pathogenesis; autoimmune disorder;
 XX neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 XX herpes virus infection; pox virus infection; adenovirus infection;
 XX proliferative disease.

XX Homo sapiens.

OS W0200226968-A2.

PN 04-APR-2002.

PD 27-SEP-2001; 2001WO-CM001379.

PF 28-SEP-2000; 2000US-00672717.

PR (UYOT-) UNIV OTTAWA.

PA (ABGE-) AEGERA THERAPEUTICS INC.

PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI: 2002-479562/51.

DR N-PSDB; ABK93869.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 XX apoptosis in a cell, for treating cancer and other proliferative
 XX diseases.

PS Example 12; Fig 1; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 XX nucleic acid (i) that inhibits IAP biological activity, regardless of
 XX length of the antisense nucleic acid, the IAP proteins may be mouse or
 XX human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 XX composition comprising a mammalian IAP antisense molecule and a method of
 XX enhancing apoptosis in a cell, comprising administering a negative
 XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 XX antisense inhibitor is useful for enhancing apoptosis in a cell in a
 XX mammal diagnosed with a proliferative disease. The method is useful for
 XX treating a patient diagnosed with a proliferative disease like cancer.

XX The IAP antisense molecule is useful to treat, ameliorate, improve,
 XX sustain or prevent proliferative diseases (e.g. ovarian cancer,
 XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 XX conditions where apoptosis is involved or implicated (e.g. embryonic
 XX development, viral pathogenesis, autoimmune disorders, neurodegenerative
 XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 XX virus, pox virus and adenovirus). The present sequence is a human IAP

CC protein sequence
XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 5; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 16
ADB80961
ID ADB80961 standard; protein; 497 AA.

AC ADB80961;
DT 04-DEC-2003 (first entry)

DE RING-SH complex related protein, SEQ ID No 35.

XX RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KM Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UTM; GTPase; E2 enzyme; Csg101;
KM cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KM rhadovirus; filovirus.

XX Unidentified.

PN W0203033646-A2.

PD 24-APR-2003.

PF 31-JUL-2002; 2002MO-US024589.

PR 31-JUL-2001; 2001US-0308958P.

PR 09-NOV-2001; 2001US-0345846P.

PA (PROT-) PROTEOLOGICS INC.

PI Greener T, Moskowitz H, Reiss Y, Alroy I;

DR WPI; 2003-393509/37.

DR N-PSDB; ADB81002.

XX New isolated protein complex comprising a RING-SH 3 polypeptide and
PT another polypeptide, useful for detecting cells infected with a virus,
PT and for treating viral disorders caused by retroviruses, rhadoviruses,
PT or filoviruses.

PS Disclosure; Fig 35; 176pp; English.

XX The invention relates to a novel isolated protein complex comprising a
CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
CC STAM2B, VHS-UTM, a GTPase, an E2 enzyme, Csg101, a cullin, RING-SH, and a
CC clathrin. The novel protein complex has virucide activity and can be used
CC to treat disorders as part of a vaccine. The protein complex and
CC composition are useful for detecting cells infected with a virus, for
CC identifying agents having antiviral activity, and for treating viral
CC disorders caused by retroviruses, rhadoviruses, or filoviruses. This
CC sequence is a protein comprising the RING-SH complex of the invention.

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 7; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 17
ADI39804
ID ADI39804 standard; protein; 497 AA.

AC ADI39804;

DT 15-APR-2004 (first entry)

DE Human inhibitor of apoptosis-like protein (IIP).

XX Inhibitor of apoptosis-like protein; IAP; IIP; apoptosis; therapy;
KM cancer; cell immortalisation; cysteine protease; viral infection;
KM cytosolic; virucide; human.

XX Homo sapiens.

OS US6511828-B1.

PN 28-JAN-2003.

PD 31-MAY-1996; 96US-00657759.

PR 31-MAY-1996; 96US-00657759.

PA (ARCH-) ARCH DEV CORP.

PI Thompson CB, Duckett CS;

DR WPI; 2003-391256/37.

XX New inhibitor of apoptosis-like protein (IIP) and polynucleotide encoding
PT IIP, useful for inhibiting or stimulating apoptosis in target cells,
PT treating certain cancers, or sustaining host cell survival following
PT viral infection.

PS Claim 1; SEQ ID NO 2; 42pp; English.

XX The present invention relates to inhibitor of apoptosis (IAP)-like
CC proteins (IIP) and polynucleotides encoding such proteins. Sequences of
CC the invention are useful for inhibiting or stimulating apoptosis in
CC target cells or for treating certain cancers. They are also useful in the
CC immortalisation of cells for culture, for inhibiting the activation of
CC cysteine proteases and to sustain host cell survival following viral
CC infection. The IIP may also be used as a marker in gel separation
CC procedures or as a standard in protein concentration determinations. The
CC present sequence is human inhibitor of apoptosis-like protein.

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 7; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 18

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ADH74639
ID ADH74639 standard; protein; 497 AA.
XX
XX ADH74639;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human XIAP polypeptide.
DE
XX Biomarker; prostate neoplastic condition; inhibitor of apoptosis; IAP;
XX XIAP; X chromosome-linked inhibitor of apoptosis; ciAP1; ciAP2;
XX prostate cancer; human.
XX
XX Homo sapiens.
OS
XX US2003224399-A1.
XX
XX 04-DEC-2003.
XX
XX 12-FEB-2003; 2003US-00366307.
XX
XX 12-FEB-2002; 2002US-0356956P.
XX
XX (REED/) REED J C.
XX PA (KRAU/) KRAJEWSKI S.
XX
XX Reed JC, Krajewski S;
XX
XX WPI; 2004-141816/14.
XX DR N-PSDB; ADH74638.
XX
XX Identifying biomarker that is diagnostic for survival of a patient with
XX PT prostate neoplastic condition by measuring level of integrin associated
XX PT protein in sample, and identifying correlation of the level in sample.
XX
XX Disclosure; SEQ ID NO 2; 42pp; English.
XX
XX The present invention relates to a method for identifying a biomarker
XX CC that is diagnostic for the survival of patient with a prostate neoplastic
XX CC condition. The method comprises measuring the level of inhibitor of
XX CC apoptosis (IAP) polypeptide chosen from chosen from XIAP (X chromosome-
XX CC linked inhibitor of apoptosis), ciAP1 and ciAP2 in a neoplastic prostate
XX CC cell-containing sample from patients, and identifying correlation between
XX CC the level of IAPs in the sample, where the correlation of an IAP with
XX CC survival in the patients indicates IAP as a biomarker diagnostic. The
XX CC method is useful for the prognosis of prostate neoplastic conditions such
XX CC as prostate cancer. The method is efficient in determining the prognosis
XX CC while the patient is still at an early stage of disease, and in
XX CC monitoring the effectiveness of a particular treatment in a prostate
XX CC neoplastic condition. The present sequence represents human XIAP.
XX
XX Sequence 497 AA;
SQ
Query Match 94.8%; Score 366; DB 8; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMDQAKCY 60
DB 265 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMDQAKCY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330
QY
DB
RESULT 19
ADL70166
ID ADL70166 standard; protein; 497 AA.
XX
XX ADL70166;
AC
XX
XX 20-MAY-2004 (first entry)
DT

```

```

XX
XX Human X chromosome linked inhibitor of apoptosis (XIAP) .
DE
XX Human; inhibitor of apoptosis; IAP; XIAP; Hodgkin's disease; cytostatic;
XX gene therapy; gene silencing.
XX
XX Homo sapiens.
XX
XX WO2004017991-A1.
XX
XX 04-MAR-2004.
XX
XX 18-JUL-2003; 2003WO-EP007889.
XX
XX 13-AUG-2002; 2002DE-01037139.
XX
XX (CELL-) CELL CENT COLOGNE GMBH.
XX
XX Kroenke M, Kaashkar H, Hamilton-Dutoit SJ, Uerigensmeier JM;
XX
XX WPI; 2004-226745/21.
XX DR N-PSDB; ADL70165.
XX
XX Using inhibitors of apoptosis-inhibitor for preparation of pharmaceutical
XX PT composition for treatment of Hodgkin's lymphomas.
XX
XX Claim 11; SEQ ID NO 2; 61pp; English.
XX
XX The present sequence is the protein sequence of human X chromosome linked
XX CC inhibitor of apoptosis (XIAP). The invention is based on the discovery
XX CC that IAPs, e.g. XIAP, are constitutively overexpressed in both Hodgkin's
XX CC lymphoma (HL)-derived B-cell lines and in primary HL tissues, and that in
XX CC B-cell lines they are associated with and inhibit in particular caspase-
XX CC 3. Based on this finding, the invention provides a new therapy of HL,
XX CC which is based on inhibitors of IAPs, especially XIAP, that reduce or
XX CC eliminate the caspase inhibiting activity. The approach leads to the
XX CC restoration of apoptotic mechanisms, which result in an increased number
XX CC of cell death events in malignant HL cells. Since IAPs, in particular
XX CC XIAP, are not overexpressed in normal tissues, the approach provides a
XX CC selective therapy for HL. Suitable IAP inhibitors include molecules that
XX CC reduce the level of IAP mRNA, reduce the level of the IAP, inhibit the
XX CC binding of the IAP to a caspase or reduce the biological activity of the
XX CC IAP, e.g. an antisense nucleic acid, short interfering RNA (siRNA),
XX CC ribozyme, anti-IAP antibody, anti-IAP aptamer, small molecule, peptide or
XX CC peptidomimetic. Diagnostic methods for the detection of HL using IAP
XX CC specific agents are also provided.
XX
XX Sequence 497 AA;
SQ
Query Match 94.8%; Score 366; DB 8; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMDQAKCY 60
DB 265 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMDQAKCY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330
QY
DB
RESULT 20
ADP23982
ID ADP23982 standard; protein; 497 AA.
XX
XX ADP23982;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX PRO polypeptide SEQ ID NO:1160.
XX
XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX

```

KW osteopathic; antidiabetic; dermatological; antipsoriatic; anti-allergic;
 KM antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
 OS Unidentified.
 XX
 XX WO2004041170-A2.
 PN
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;
 PI Mu TD;
 XX WPI; 2004-419628/39.
 DR N-PSDB; ADP23981.
 XX
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 1160; 2940bp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC anti-inflammatory, antiallergic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, anti-allergic,
 CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthritis, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 XX
 SQ Sequence 497 AA;
 Query Match 94.8%; Score 366; DB 8; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGKCFHCGGGLTDWKPSPDPMDQNAKCY 60
 DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGKCFHCGGGLTDWKPSPDPMDQNAKCY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

ID AAM19745 standard; protein; 496 AA.
 XX
 XX AAM19745;
 AC
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Mouse inhibitor of apoptosis protein homologue MIMA.
 XX
 KM Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIMA;
 KM degenerative disease; infectious disease; autoimmune disease; cancer;
 KM therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 XX
 FH Key Location/Qualifiers
 FT Region 26..93
 FT /label= BIR
 FT 163..230
 FT /label= BIR
 FT 264..330
 FT /label= BIR
 FT Region 448..485
 FT /label= RING_finger
 FT
 PN WO9723501-A1.
 XX
 PD 03-JUL-1997.
 XX
 PF 20-DEC-1996; 96WO-AU000827.
 XX
 PR 22-DEC-1995; 95AU-00007275.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Vaux DL;
 XX
 XX WPI; 1997-350966/32.
 DR N-PSDB; AAT72710.
 XX
 PT Isolated protein homologues of viral inhibitors of apoptosis - used to
 PT modulate apoptosis for treatment of degenerative, infectious or
 PT auto-immune diseases and cancer.
 PT
 PS Claim 7; Page 44-47; 136pp; English.
 XX
 CC Mammalian IAP homologue A (MIMA) (AAM19745) is a murine homologue of
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence
 CC was deduced from a cDNA clone (see also AAT72710) isolated from a mouse
 CC liver cDNA library on the basis of homology to Oryzias pseudotsuguta
 CC polyhedrosis virus IAP BIR and RING finger amino acid motifs (see also
 CC AAM19744). IAP homologues (see also AAM19746-52) and their derivatives
 CC and chemical analogues can be used in methods for modulating apoptosis in
 CC animal cells, specifically for treatment, by inhibition, of degenerative
 CC and infectious disease or, by promotion, of cancer and autoimmune disease
 CC
 XX
 SQ Sequence 496 AA;
 Query Match 92.5%; Score 357; DB 2; Length 496;
 Best Local Similarity 93.9%; Pred. No. 8.6e-36;
 Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGKCFHCGGGLTDWKPSPDPMDQNAKCY 60
 DB 264 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGKCFHCGGGLTDWKPSPDPMDQNAKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 21
 AAM19745

RESULT 22
 ADB61820
 ID ADB61820 standard; protein; 66 AA.

XX ADB61820;
AC 04-DEC-2003 (first entry)
DT
XX
DE Human inhibitor of apoptosis (IAP) protein testis IAP BIR2 domain.
XX
KM baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM H1AP1; CIAP2; H1AP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytoskeletal; neoplasm; leukemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms' tumor; human; BIR 2 domain.
XX
OS Homo sapiens.
XX
PN WO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
XX 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Boudreault A, Korneluk RG, La Casse E, Liston P;
XX
DR WPI; 2003-513532/48.
XX
PT Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating a
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1A; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1
CC (CIAP2) and H1AP2 (CIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilms' tumor, and for enhancing apoptosis. The present sequence is
CC that of the human inhibitor of apoptosis (IAP) protein testis IAP BIR2
CC domain which was used to demonstrate homology to other human IAP protein
CC BIR domains to which the peptides of the invention are targeted to bind.
XX
SQ Sequence 66 AA:
Query Match 86.5%; Score 334; DB 7; Length 66;
Best Local Similarity 81.8%; Pred. No. 6.3e-34;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
1 YEARLITFTGWTMYSVNKEQLARAGFYALSGDVKVCKHCGGGLTDMKPSDDPDQAKCY 60

Db 1 YEARLITFTGWTMYSVNKEQLARAGFYALSGEDHYOCFCHCGGLANWKPKEDPWEQHAQWY 60
Oy 61 PGCKYL 66
Db 61 PGCKYL 66
RESULT 23
ID AAY81440 standard; protein; 236 AA.
XX
AC AAY81440;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human TIAP (an inhibitor of apoptosis).
XX
KM TIAP, inhibitor of apoptosis protein; IAP; X-linked IAP; XIAP;
KM internal ribosome entry site; IRES; human; cap-independent translation;
KM drug screening; cancer; autoimmune disease; degenerative disease;
KM immunorejection; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00123979.
XX 14-JUN-1999; 99US-00332319.
XX
PA (UYOF-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
XX
DR WPI; 2000-338644/29.
DR N-FSDB; AAA06940.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 82; 87pp; English.
XX
CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining the
CC amount of translation from the XIAP IRES reporter cistron exposed to the
CC compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation from the exposed
CC XIAP IRES reporter cistron indicates a compound that increases XIAP IRES-
CC dependent (cap independent) translation. XIAP protein plays a critical
CC role in the regulation of apoptosis by suppressing activation of
CC downstream caspase-3 and caspase-7. Compounds identified by the method
CC which decrease XIAP IRES-dependent translation (thus leading to reduced
CC expression of XIAP and hence increasing apoptosis) can be used for
CC treating cancer. The methods can also be used for the identification of
CC agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP; AAY81440). Such constructs may be used in
CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents human TIAP (an inhibitor of apoptosis protein), DNA encoding
CC which may be used in an expression vector comprising a XIAP IRES element

```

XX          Sequence 236 AA;
SQ
Query Match      86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY          1 YEARIVTGTWIVSYVNEKQLARAGFYALGEGDVKYKCFHGGGGLTDMKPSDPMQDAKCY 60
           |||||
           4 YEARLITFGTWMYSVNEKQLARAGFYALGEGDVKYKCFHGGGGLANMKPKEDPMQDAKMY 63

QY          61 PGCKYTL 66
           |||||
           64 PGCKYTL 69

Db
Query Match      86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

RESULT 24
AAE00365
ID AAE00365 standard; protein; 236 AA.
XX
AC AAE00365;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
XX
KM Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KM chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
KM TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KM cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KM T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KM retinal degeneration; hyperferritinemia-cataract syndrome; cancer;
KM autoimmune disease; diabetes; multiple sclerosis; cyrostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 7..70
           /label= "BIR domain
           /note= "Baculovirus iap repeat"
FT Domain 188..223
           /label= RING_finger_domain

W0200123568-A2.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US026735.
XX
PR 30-SEP-1999; 99US-0157169P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Duckett C, Mir SS;
XX
DR WPI: 2001-258135/26.
XX
DR N-PSDB; AAD03581.
XX
PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis.
XX
PS Claim 1; Fig 2; 108pp; English.
XX
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC (ILP-2). The hILP-2 gene is located on chromosome 19q13.3-q13.4. ILP-2
CC comprises a single amino-terminal domain known as baculovirus iap repeat
CC (BIR), followed by a spacer region and a carboxy-terminal ring finger
CC domain. It interacts with transforming growth factor beta receptor
CC (TGFbetaR) and modulates TGFbetaR activity. It also potentially inhibits
CC apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It
CC also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in

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CC the area of genetic testing for predisposition to diseases, such as cone-
CC rod retinal dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell
CC acute lymphoblastic leukaemia, colorectal cancer and hyperferritinemia-
CC cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also
CC used in the treatment of diseases associated with abnormal apoptosis such
CC as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
CC neurodegenerative diseases including retinal degeneration. The ILP-2 gene
CC is also used in gene therapy for treating patients suffering from ILP-2
CC gene deletions or mutations
XX
SQ          Sequence 236 AA;
Query Match      86.5%; Score 334; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY          1 YEARIVTGTWIVSYVNEKQLARAGFYALGEGDVKYKCFHGGGGLTDMKPSDPMQDAKCY 60
           |||||
           4 YEARLITFGTWMYSVNEKQLARAGFYALGEGDVKYKCFHGGGGLANMKPKEDPMQDAKMY 63

QY          61 PGCKYTL 66
           |||||
           64 PGCKYTL 69

Db
Query Match      86.5%; Score 334; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

RESULT 25
AAU75066
ID AAU75066 standard; protein; 236 AA.
XX
AC AAU75066;
XX
DT 23-APR-2002 (first entry)
XX
DE Human testes specific inhibitor of apoptosis (TIAP) protein.
XX
KM TIAP; apoptosis; testes specific inhibitor of apoptosis; human;
KM apoptotic; cytosolic; anti-infertility; contraceptive;
KM chromosome 12q22-23; transgenic animal; antibody; immunogen;
KM testicular cell; testicular cancer; cancer; male infertility;
KM male birth control; XIAP.
XX
OS Homo sapiens.
XX
PN US6331412-B1.
XX
PD 18-DEC-2001.
XX
PF 29-JAN-1999; 99US-00239867.
XX
PR 29-JAN-1998; 98US-0073001P.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Lagace M;
XX
DR WPI: 2002-105275/14.
XX
DR N-PSDB; ABK3197.
XX
PT Nucleic acids encoding a testis specific apoptosis inhibitor protein
PT (TIAP) useful for treating testicular cancers, cancers in non-testicular
PT tissues, male infertility, and for achieving male birth control.
XX
PS Example 4; Fig 4B; 29pp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a TIAP polypeptide (testes-specific inhibitor of apoptosis) protein. This
CC gene is a homologue of the X-linked XIAP gene and is located on
CC chromosome 12q22-23. The nucleotide and protein sequences of the
CC invention and vectors containing these sequences may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC be used to express the TIAP protein by recombinant methods. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate

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XX WPI; 2004-651687/63.
DR
XX
PT New isolated BIR domain binding (BDB) oligopeptide that specifically
PT binds melanoma inhibitor of apoptosis (ML-IAP) and releases the
PT inhibitory effect that ML-IAP has on caspase activity, useful for
PT increasing apoptosis in cells.
XX
PS Example 10; Fig 5; 50pp; English.
XX
XX The invention describes an isolated BIR domain binding (BDB) oligopeptide
CC that specifically binds melanoma inhibitor of apoptosis (ML-IAP) and
CC releases the inhibitory effect that ML-IAP has on caspase activity. Also
CC described are: a method of increasing apoptosis in a cell comprising
CC contacting the cell with the oligopeptide, where the apoptosis is
CC increased; an article of manufacture comprising a container; the
CC composition of matter contained within the container; and a label affixed
CC to the container, or a package insert included with the container,
CC referring to the use of the composition of matter for the therapeutic
CC treatment of or the diagnostic detection of a cancer; a method of
CC screening antagonists of IAP polypeptides comprising co-crystallising the
CC potential antagonist with the Baculovirus IAP repeat (BIR) domain of an
CC ML-IAP polypeptide to form a co-crystalline structure and determining if
CC the potential antagonist binds to the BIR domain; determining whether the
CC antagonist increases apoptosis in cells relative to antagonist untreated
CC cells; a method of screening antagonists of an ML-IAP polypeptide
CC comprising co-crystallising the potential antagonist with the BIR domain
CC of an ML-IAP polypeptide to form a co-crystalline structure and
CC determining if the potential antagonist binds to the BIR domain, and
CC where binding occurs if there is at least one contact between a specific
CC amino acid residue of a given patch and the candidate molecule that is
CC less than or equal to 2.8 angstroms in the co-crystalline structure. The
CC oligopeptide and composition of matter are useful for increasing
CC apoptosis in cells, preferably cancer cells such as a melanoma cell, a
CC breast cancer cell, a colorectal cancer cell, a lung cancer cell, an
CC ovarian cancer cell, a central nervous system cancer cell, a liver cancer
CC cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer
CC cell, and a leukaemia cell. This is the amino acid sequence of IAP BIR
CC domain associated with the selection of BIR domain binding oligopeptides.
XX
SQ Sequence 87 AA;
Query Match 84.6%; Score 326.5; DB 8; Length 87;
Best Local Similarity 87.9%; Pred. No. 7.6e-33;
Matches 56; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
QY 1 YEARIIVFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 60
DB 9 YEARKXTFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 67
QY 61 PGCKYL 66
DB 68 PGCKYL 73
XX
DE RESULT 30
ID ADB61831 standard; protein; 66 AA.
XX
AC ADB61831;
XX
DT 04-DEC-2003 (first entry)
XX
XX Gorilla inhibitor of apoptosis (IAP) protein IAP BIR3 domain.
XX
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative diseases; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis IAP; XIAP;
KM HIAP1; GIAP2; HIAP2; GIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytostatic; neoplasia; leukaemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;

KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; BIR 3 domain; gorilla.
XX
XX Gorilla gorilla.
OS
XX WC02003040172-A2.
FN
XX
PD 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-CA001738.
PF
XX
PR 09-NOV-2001; 2001US-033230P.
PR 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Boudreau A, Korneluk RG, La Caease B, Lileton P;
XX
DR WPI; 2003-513532/48.
XX
XX Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.
XX
XX This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (GIAP2) and HIAP2 (GIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the gorilla inhibitor of apoptosis (IAP) protein IAP BIR3 domain
CC to which the peptides of the invention are targeted to bind.
XX
SQ Sequence 66 AA;
Query Match 84.2%; Score 325; DB 7; Length 66;
Best Local Similarity 78.8%; Pred. No. 8.4e-33;
Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 YEARIIVFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 60
DB 1 YEAMWLTFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66
XX
DE RESULT 31
ID AAE00367 standard; protein; 236 AA.
XX
AC AAE00367;
XX
DT 19-JUN-2001 (first entry)

XX DE Gorilla IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
 XX XX
 KM Gorilla; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
 KM transforming growth factor beta receptor; TGFbetaR; cytosolic;
 KM c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
 KM cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
 KM T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 KM retinal degeneration; hyperferritinemia-cataract syndrome; cancer;
 KM autoimmune disease; diabetes; multiple sclerosis.
 XX
 OS Gorilla gorilla.
 XX
 PN W0200123568-A2.
 XX
 PD 05-APR-2001.
 XX
 PD 29-SEP-2000; 2000WO-US026735.
 XX
 PR 30-SEP-1999; 99US-0157169P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PT Duckert C, Mir SS;
 XX
 DR WPI; 2001-258135/26.
 XX
 DR N-PSDB; AAD03583.
 XX
 PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
 PT transforming growth factor beta receptor modulating activity, and the
 PT nucleic acids that encode them, useful for treating, e.g. diabetes and
 PT multiple sclerosis.
 XX
 PS Claim 1; Fig 2; 108bp; English.
 XX
 CC The present sequence is gorilla inhibitor of apoptosis (IAP)-like protein
 CC -2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain known as
 CC baculovirus iap repeat (BIR), followed by a spacer region and a carboxy-
 CC terminal ring finger domain. It interacts with transforming growth factor
 CC beta receptor (TGFbetaR) and modulates TGFbetaR activity. It also
 CC potentially inhibits apoptosis induced by overexpression of Bax or by
 CC Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
 CC activity. ILP-2 is used in the area of genetic testing for predisposition
 CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
 CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
 CC and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or
 CC mutation. The ILP is also used in the treatment of diseases associated
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
 CC diabetes and multiple sclerosis and neurodegenerative diseases including
 CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
 CC treating patients suffering from ILP-2 gene deletions or mutations
 CC
 XX
 SQ Sequence 236 AA;
 Query Match 84.2%; Score 325; DB 4; Length 236;
 Best Local Similarity 79.8%; Pred. No. 3.7e-32;
 Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEARIITFGTWISYVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKCY 60
 DB 4 YEALITFGTWISYVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKCY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69
 RESULT 32
 ADB61832
 ID ADB61832 standard; protein. 57 AA.
 AC ADB61832;
 XX

DT 04-DEC-2003 (first entry)
 XX
 XX Unidentified inhibitor of apoptosis (IAP) protein IAP BIR3 domain.
 XX
 KM baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KM autoimmune disorder; neurodegenerative disease; apoptotic response;
 KM systemic lupus erythematosus; multiple sclerosis; viral infection;
 KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KM HAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KM caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KM cervical cancer; uterine cancer; testicular cancer;
 KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KM Wilms' tumor; BIR 3 domain.
 XX
 OS Unidentified.
 XX
 PN W02003040172-A2.
 XX
 PD 15-MAY-2003.
 XX
 PD 12-NOV-2002; 2002MO-CA001738.
 XX
 PR 09-NOV-2001; 2001US-0332300P.
 XX
 PR 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Boudreault A, Korneluk RG, La Casse E, Liston P;
 XX
 DR WPI; 2003-513532/48.
 XX
 PT Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating a
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1B; 53bp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example, systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAP1
 CC (CIAP2) and HAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumor, and for enhancing apoptosis. The present sequence is
 CC that of an unidentified inhibitor of apoptosis (IAP) protein IAP BIR3
 CC domain which was used to demonstrate homology to human IAP protein BIR
 CC domains to which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 57 AA;
 Query Match 79.3%; Score 306; DB 7; Length 57;
 Best Local Similarity 91.1%; Pred. No. 1.7e-30;
 Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 11 WISYVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKCYPGCKYL 66
 DB 2 WISYVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKHMGCKYL 57

	Query Match	66.8%	Score 258	DB 7	Length 52	
	Best Local Similarity	91.7%	Pred. No. 1.6e-24			
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					Gaps	0
Oy	1 YEARLVTGFWTYSVNKEQLARAGFYALGEGBKVCFCFGGLDPMKP	48				
	: : : :					
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	: : : :					
	RESULT 37					
ID	ADB61833					
XX	ADB61833 standard; protein; 68 AA.					
AC	ADB61833;					
XX						
DT	04-DEC-2003 (first entry)					
DE	zebra fish inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.					
XX						
KM	baculovirus inhibitor of apoptosis repeat domain; BIR domain;					
KM	apoptosis pathway; embryonic development; viral pathogenesis; cancer;					
KM	autoimmune disorder; neurodegenerative disease; apoptotic response;					
KM	systemic lupus erythematosus; multiple sclerosis; viral infection;					
KM	herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;					
KM	H1AP1; CIAP2; H1AP1; CIAP1; RING zinc finger; caspase-3; caspase-7;					
KM	caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;					
KM	cervical cancer; uterine cancer; testicular cancer;					
KM	small cell lung carcinoma; uterine cancer; renal cell carcinoma;					
KM	Wilms' tumour; BIR 3 domain; zebra fish.					
XX						
OS	Danio rerio.					
PN	WO2003040172-A2.					
XX						
PD	15-MAY-2003.					
XX						
PF	12-NOV-2002; 2002WO-CA001738.					
XX						
PR	09-NOV-2001; 2001US-0332300P.					
XX						
PR	08-APR-2002; 2002US-0370934P.					
XX						
PA	(AEGE-) AEGERA THERAPEUTICS INC.					
P1	Boudreault A, Korneluk RG, La Casse E, Liston P,					
DR	WPI; 2003-513532/48.					
XX						
PT	Polypeptide capable of forming a complex with a polypeptide comprising a					
PT	baculovirus inhibitor of apoptosis repeat domain useful for treating					
PT	cancer and other neoplasms.					
PS						
PS	Disclosure; Fig 1B; 53pp; English.					
CC	This invention relates to a substantially pure polypeptide having a					
CC	length of less than 100 amino acids and capable of forming a complex with					
CC	a polypeptide that includes a baculovirus inhibitor of apoptosis repeat					
CC	(BIR) domain. The apoptosis pathway is known to play a critical role in					
CC	embryonic development, viral pathogenesis, cancer, autoimmune disorders					
CC	and neurodegenerative diseases. The failure of the apoptotic response has					
CC	been implicated in the development of cancer, autoimmune disorders (for					
CC	example systemic lupus erythematosus and multiple sclerosis) and viral					
CC	infections (including herpes virus, poxvirus and adenovirus. The					
CC	inhibitors of apoptosis (IAPs) are a family of proteins possessing one or					
CC	more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1					
CC	(CIAP2) and H1AP2 (CIAP1) all possess three BIR domains and carboxy					
CC	terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and					
CC	-9 which are proteases involved in the initiation of apoptosis. Compounds					
CC	which inhibit the activity of IAPs may therefore have cytostatic activity					
CC	through the enhancement of apoptosis. The polypeptides of the invention					
CC	are candidate peptide ligands for binding to the BIR domain of IAPs. They					
CC	may be useful for the treatment of cancer and other neoplasms, such as					
CC	leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular					
CC	cancer, small-cell lung carcinoma, uterine cancer, renal cell carcinoma					

[illegible]

CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HAPI2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms tumor, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein HAPI BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

XX Sequence 68 AA;

Query Match 51.3%; Score 198; DB 7; Length 68;

Best Local Similarity 55.9%; Pred. No. 7.2e-17; Mismatches 22; Indels 2; Gaps 1;

Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIYVFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDWKPSEDPWQHA 58

Db 1 HAAAFKTFEWMPPSSVLVNPEQLASAGFYVGNSDVXKFCDCGGLRCMESGDDPWQHA 60

Qy 59 CYPGCKYL 66

Db 61 WPRRCBYL 68

RESULT 39

ADO26592 standard; protein; 442 AA.

AC ADO26592;

DT 01-JUL-2004 (first entry)

DE Human APl2.

XX Chromosome translocation; malignancy;

KW mucosa-associated lymphoid tissue-lymphoma associated translocation;

KM MLT; primary cell transformation; apoptosis inhibitor 2; APl2;

XX tumour; cytostatic; human.

OS Homo sapiens.

XX US6689875-B1.

PN 10-FEB-2004.

PD 26-MAY-2000; 2000US-00579692.

PF 09-JUN-1999; 99US-0138834P.

PR (VLAAS) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PA Dierlamm J, Baens M, Marlijnen P;

PI WPI, 2004-141430/14.

DR N-PSDB; ADO26591.

XX New mucosa-associated lymphoid tissue-lymphoma associated translocation

PT protein, useful in diagnosing and treating tumors.

PS Disclosure; SEQ ID NO 58; 88pp; English.

XX The present invention relates to a method for characterisation of

CC chromosomes translocation T (11;18) (q21;q21) and its association with

CC malignancies such as mucosa-associated lymphoid tissue (MLT)-lymphomas.

CC Also disclosed are: the polynucleotide and polypeptide sequences for

CC human mucosa-associated lymphoid tissue (MLT)-lymphoma associated

CC translocation (MLT), and a novel mechanism of primary cell transformation

CC by expression of a fusion protein comprising at least apoptosis inhibitor
 CC 2 (APl2) fused to another protein such as MLT. The MLT polynucleotide and
 CC polypeptide sequences, and the method of the invention are useful in
 CC diagnosing and treating tumors. The present sequence represents human
 CC APl2.

XX Sequence 442 AA;

Query Match 51.3%; Score 198; DB 8; Length 442;

Best Local Similarity 55.9%; Pred. No. 6.4e-16; Mismatches 22; Indels 2; Gaps 1;

Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIYVFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDWKPSEDPWQHA 58

Db 255 HAAAFKTFEWMPPSSVLVNPEQLASAGFYVGNSDVXKFCDCGGLRCMESGDDPWQHA 314

Qy 59 CYPGCKYL 66

Db 315 WPRRCBYL 322

RESULT 40

ABP72159 standard; protein; 557 AA.

AC ABP72159;

DT 22-APR-2003 (first entry)

DE Inhibitor of apoptosis protein CIAP2.

XX Inhibitor of apoptosis; CIAP2; apoptosis; cancer; leukemia; lymphoma;

KW neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX Unidentified.

XX WO2003004606-A2.

PN 16-JAN-2003.

PD 03-JUL-2002; 2002WO-US021002.

PF 03-JUL-2001; 2001US-00898158.

PR (UYCO) UNIV COLUMBIA NEW YORK.

PA Troy CM, Shelanski ML;

PI WPI, 2003-210351/20.

DR N-PSDB; ABZ58104.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

PT treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 17A; 124pp; English.

XX The present sequence is the protein sequence of inhibitor of apoptosis

CC protein CIAP2. The invention provides a nucleic acid, such as an

CC antisense oligonucleotide, which specifically hybridises to a nucleic

CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,

CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's

CC death comprises contacting the cell with the nucleic acid under

CC conditions permitting the nucleic acid to enter the cell, especially the

CC use of a vector, liposome, or a mechanical or electrical means. The

CC method is used to treat acute lymphocytic leukaemia, acute myelogenous

CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal

CC cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 557 AA;

Query Match 51.3%; Score 198; DB 6; Length 557;

Best Local Similarity 55.9%; Pred. No. 8.4e-16;

Matches	38;	Conservative	6;	Mismatches	22;	Indels	2;	Gaps	1;
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Db	255	HAARFKTFFFMPSVLVNPEQLASAGFYVGNSDVKCFCCDGLRCWESGDDPMVQAK	314						
Qy	59	CYPCKYL	66						
Db	315	WPPRCXYL	322						

Search completed: June 15, 2005, 17:35:44
 Job time : 117 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:39:48 ; Search time 108.5 Seconds
(without alignments)
233.180 Million cell updates/sec

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Perfect score: 386
Sequence: 1 YEARIYFTGWTIVSVNKEQL.....KPSDPDWDHAKCPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Published Applications AA:*
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3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	386	100.0	66 9 US-09-201-936-24	Sequence 24, App1
2	386	100.0	66 16 US-10-600-272-24	Sequence 24, App1
3	386	100.0	496 9 US-09-974-592-10	Sequence 10, App1
4	386	100.0	496 9 US-09-201-936-10	Sequence 10, App1
5	386	100.0	496 16 US-10-636-065-225	Sequence 225, App1
6	386	100.0	496 16 US-10-600-272-10	Sequence 10, App1
7	372	96.4	496 16 US-10-482-952-5	Sequence 5, App1
8	366	94.8	66 9 US-09-201-936-25	Sequence 25, App1
9	366	94.8	66 16 US-10-600-272-25	Sequence 25, App1
10	366	94.8	107 9 US-09-965-967-20	Sequence 20, App1
11	366	94.8	236 13 US-10-024-433-4	Sequence 4, App1

12	366	94.8	278 9 US-09-964-899-39	Sequence 39, App1
13	366	94.8	497 9 US-09-974-592-4	Sequence 4, App1
14	366	94.8	497 9 US-09-201-936-4	Sequence 4, App1
15	366	94.8	497 15 US-10-366-307-2	Sequence 2, App1
16	366	94.8	497 16 US-10-636-065-219	Sequence 219, App1
17	366	94.8	497 16 US-10-600-272-1	Sequence 4, App1
18	334	86.5	236 13 US-10-024-433-2	Sequence 2, App1
19	334	86.5	464 15 US-10-343-115-2	Sequence 2, App1
20	233	60.4	50 14 US-10-138-618-28	Sequence 28, App1
21	233	60.4	50 14 US-10-138-618-29	Sequence 29, App1
22	233	60.4	50 14 US-10-138-618-32	Sequence 32, App1
23	198	51.3	68 9 US-09-201-936-26	Sequence 26, App1
24	198	51.3	16 US-10-600-272-26	Sequence 26, App1
25	198	51.3	557 16 US-10-482-952-9	Sequence 9, App1
26	198	51.3	604 9 US-09-974-592-6	Sequence 6, App1
27	198	51.3	604 9 US-09-201-936-6	Sequence 6, App1
28	198	51.3	604 14 US-10-232-286-4	Sequence 4, App1
29	198	51.3	604 14 US-10-141-618-6	Sequence 6, App1
30	198	51.3	604 15 US-10-366-307-6	Sequence 6, App1
31	198	51.3	604 16 US-10-636-065-221	Sequence 221, App1
32	198	51.3	604 16 US-10-600-272-6	Sequence 6, App1
33	198	51.3	604 16 US-10-730-476A-79	Sequence 79, App1
34	198	51.3	604 16 US-10-825-282-40	Sequence 40, App1
35	198	51.3	604 17 US-10-934-717-4	Sequence 4, App1
36	198	51.3	1140 14 US-10-353-461-8	Sequence 8, App1
37	190	49.2	68 9 US-09-201-936-28	Sequence 28, App1
38	190	49.2	68 14 US-10-041-859-18	Sequence 18, App1
39	190	49.2	68 16 US-10-600-272-28	Sequence 28, App1
40	190	49.2	172 14 US-10-041-859-12	Sequence 12, App1
41	190	49.2	268 14 US-10-323-643-10	Sequence 10, App1
42	189	49.0	600 9 US-09-974-592-12	Sequence 12, App1
43	189	49.0	600 16 US-10-482-952-1	Sequence 1, App1
44	185	47.9	68 14 US-10-041-859-14	Sequence 14, App1
45	185	47.9	172 14 US-10-041-859-8	Sequence 8, App1

ALIGNMENTS

RESULT 1
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication NO. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-201-936-24
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Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 66; Conservative 0; Mismatches 0; Gaps 0;

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US-10-600-272-24
; Sequence 24, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-600-272-24

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Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY      61 PGCKYL 66
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RESULT 3
US-09-974-592-10
; Sequence 10, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13

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; NUMBER OF SEQ ID NOS: 17
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; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRF
; ORGANISM: Mus musculus
US-09-974-592-10

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Db     324 PGCKYL 329
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: Publication No. US20020187946A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: TITLE OF INVENTION: PROBES, AND DETECTION METHODS
: FILE REFERENCE: 07891/003003
: CURRENT APPLICATION NUMBER: US/09/201,936
: EARLIER FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: 09/011,356
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 496
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-201-936-10

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Query Match      100.0%; Score 386; DB 9; Length 496;
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RESULT 5
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; Sequence 225, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin

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APPLICANT: Young, Sean
 TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
 FILE REFERENCE: 07891/025005
 CURRENT APPLICATION NUMBER: US/10/636,065
 PRIOR FILING DATE: 2003-08-07
 PRIOR APPLICATION NUMBER: 09/672,717
 NUMBER OF SEQ ID NOS: 231
 SOFTWARE: FastSeq for Windows Version 4.0
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 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-636-065-225

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QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 6
 US-10-600-272-10
 Sequence 10, Application US/10600272
 Publication No. US20040157232A1
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 APPLICANT: Liston, Peter
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 FILE REFERENCE: 07891/003006
 CURRENT APPLICATION NUMBER: US/10/600,272
 CURRENT FILING DATE: 2003-06-20
 PRIOR APPLICATION NUMBER: US 09/011,356
 PRIOR FILING DATE: 1998-02-04
 PRIOR APPLICATION NUMBER: PCT/IB96/01022
 PRIOR FILING DATE: 1996-08-05
 PRIOR APPLICATION NUMBER: US 08/576,956
 PRIOR FILING DATE: 1995-12-22
 PRIOR APPLICATION NUMBER: US 08/511,485
 PRIOR FILING DATE: 1995-08-04
 NUMBER OF SEQ ID NOS: 45
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 Best Local Similarity 100.0%; Pred. No. 1e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 7

US-10-482-952-5
 Sequence 5, Application US/10482952
 Publication No. US20040254136A1
 GENERAL INFORMATION:
 APPLICANT: The Trustees of Columbia University in the City of New York, et al.
 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CELL
 FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
 CURRENT APPLICATION NUMBER: US/10/482,952
 CURRENT FILING DATE: 2004-01-05
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5
 LENGTH: 496
 TYPE: PRT
 ORGANISM: human
 US-10-482-952-5

Query Match 96.4%; Score 372; DB 16; Length 496;
 Best Local Similarity 97.0%; Pred. No. 5.3e-37;
 Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 8
 US-09-201-936-25
 Sequence 25, Application US/09201936
 Publication No. US20020187946A1
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 APPLICANT: Liston, Peter
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 FILE REFERENCE: 07891/003003
 CURRENT APPLICATION NUMBER: US/09/201,936
 CURRENT FILING DATE: 1998-12-01
 PRIOR APPLICATION NUMBER: 09/011,356
 PRIOR FILING DATE: 1998-02-04
 PRIOR APPLICATION NUMBER: PCT/IB96/01022
 PRIOR FILING DATE: 1996-08-05
 PRIOR APPLICATION NUMBER: US 08/576,956
 PRIOR FILING DATE: 1995-12-22
 PRIOR APPLICATION NUMBER: US 08/511,485
 PRIOR FILING DATE: 1995-08-04
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 25
 LENGTH: 66
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-201-936-25

Query Match 94.8%; Score 366; DB 9; Length 66;
 Best Local Similarity 95.5%; Pred. No. 3.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 60
 DB 1 YEARIYFTGWTISVVKNEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMDOHAKCY 60

QY 61 PGCKYL 66
 DB 61 PGCKYL 66

```
RESULT 9
US-10-600-272-25
; Sequence 25, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-25
```

```
Query Match          94.8%; Score 366; DB 16; Length 66;
Best Local Similarity 95.5%; Pred. No. 3,4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKMY 60
```

```
Qy 61 PGCKYL 66
Db 61 PGCKYL 66
```

```
RESULT 10
US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: FU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20
```

```
Query Match          94.8%; Score 366; DB 9; Length 107;
Best Local Similarity 95.5%; Pred. No. 5,7e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 15 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKMY 74
```

```
Qy 61 PGCKYL 66
Db 75 PGCKYL 80
```

```
RESULT 11
US-10-024-433-4
; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-4
```

```
Query Match          94.8%; Score 366; DB 13; Length 236;
Best Local Similarity 95.5%; Pred. No. 1,3e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 4 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKMY 63
```

```
Qy 61 PGCKYL 66
Db 64 PGCKYL 69
```

```
RESULT 12
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39
```

```
Query Match          94.8%; Score 366; DB 9; Length 278;
Best Local Similarity 95.5%; Pred. No. 1,6e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 46 YEARIVTFTGWTIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDMKPSDPMDOHAKMY 105
```

```
Qy 61 PGCKYL 66
Db 106 PGCKYL 111
```

RESULT 13
US-09-974-592-4
Sequence 4, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 14
US-09-201-936-4
Sequence 4, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCR/1896/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 15
US-10-366-307-2
Sequence 2, Application US/10366307
Publication No. US20030224399A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: Method for Determining the Prognosis
TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
FILE REFERENCE: P-LJ 5659
CURRENT APPLICATION NUMBER: US/10/366,307
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 60/356,956
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-10-366-307-2

Query Match 94.8%; Score 366; DB 15; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 16
US-10-636-065-219
Sequence 219, Application US/10636065
Publication No. US20040127694A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Theracof
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 219
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-10-636-065-219

```
Query Match          94.8%; Score 366; DB 16; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 17
US-10-600-272-4
; Sequence 4, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-4

Query Match          94.8%; Score 366; DB 16; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 18
US-10-024-433-2
; Sequence 2, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-2

Query Match          86.5%; Score 334; DB 13; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.1e-32;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
Db 4 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLANMKPKEDPMDOHAKMY 63
Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 19
US-10-343-115-2
; Sequence 2, Application US/10343115
; Publication No. US20040072999A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: Novel inhibitor of apoptosis protein
; FILE REFERENCE: IAPL-7BHW5
; CURRENT APPLICATION NUMBER: US/10/343,115
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-115-2

Query Match          86.5%; Score 334; DB 15; Length 464;
Best Local Similarity 81.8%; Pred. No. 2.3e-32;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
Db 232 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLANMKPKEDPMDOHAKMY 291
Qy 61 PGCKYL 66
Db 292 PGCKYL 297

RESULT 20
US-10-138-618-28
; Sequence 28, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/975,080
 FILING DATE: 20-NOV-1997
 APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-10-138-618-28

Query Match 60.4%; Score 233; DB 14; Length 50;
 Best Local Similarity 95.0%; Pred. No. 5.7e-21;
 Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 66
 Db 1 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 40

RESULT 21
 US-10-138-618-29
 ; Sequence 29, Application US/10138618
 ; Publication No. US20030100525A1
 ; GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 CELLULAR APOPTOSIS, AND ITS MODULATION
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/138,618
 FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/975,080
 FILING DATE: 20-NOV-1997
 APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 50 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-10-138-618-29

Query Match 60.4%; Score 233; DB 14; Length 50;
 Best Local Similarity 95.0%; Pred. No. 5.7e-21;
 Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 66
 Db 1 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 40

RESULT 22
 US-10-138-618-32
 ; Sequence 32, Application US/10138618
 ; Publication No. US20030100525A1
 ; GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 CELLULAR APOPTOSIS, AND ITS MODULATION
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/138,618
 FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/975,080
 FILING DATE: 20-NOV-1997
 APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
 LENGTH: 50 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-10-138-618-32

Query Match 60.4%; Score 233; DB 14; Length 50;
 Best Local Similarity 95.0%; Pred. No. 5.7e-21;
 Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 66
 Db 1 ALGEGDKVKCFHCGGGLTDWKPSEDPMDOHAKCYPGCKYL 40

RESULT 23
 US-09-201-936-26
 ; Sequence 26, Application US/09201936
 ; Publication No. US20020187946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26

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Query Match          51.3%; Score 198; DB 9; Length 68;
Best Local Similarity 55.9%; Pred. No. 1.6e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

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QY 1 YEARIVTFTWIVS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
Db 1 HAARFKTFPMWPSVLYNPEQLASAGFYVGNSDVYKFCDDGLRCWESGDDPMVQHAH 60

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QY 59 CYPCCKYL 66
Db 61 WPPRCXYL 68

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RESULT 24
US-10-600-272-26
; Sequence 26, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-26

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Query Match          51.3%; Score 198; DB 16; Length 68;
Best Local Similarity 55.9%; Pred. No. 1.6e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
QY 1 YEARIVTFTWIVS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58

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Db 1 HAARFKTFPMWPSVLYNPEQLASAGFYVGNSDVYKFCDDGLRCWESGDDPMVQHAH 60
QY 59 CYPCCKYL 66
Db 61 WPPRCXYL 68

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RESULT 25
US-10-482-952-9
; Sequence 9, Application US/10482952
; Publication No. US20040254136A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York, et al.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CELL
; FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
; CURRENT APPLICATION NUMBER: US/10/482,952
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 9
; LENGTH: 557
; TYPE: PRT
; ORGANISM: human
US-10-482-952-9

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Query Match          51.3%; Score 198; DB 16; Length 557;
Best Local Similarity 55.9%; Pred. No. 1.5e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

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QY 1 YEARIVTFTWIVS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
Db 255 HAARFKTFPMWPSVLYNPEQLASAGFYVGNSDVYKFCDDGLRCWESGDDPMVQHAH 314

```

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QY 59 CYPCCKYL 66
Db 315 WPPRCXYL 322

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RESULT 26
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; APPLICANT: Bairst, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6

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Query Match          51.3%; Score 198; DB 9; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
QY 1 YEARIVTFTWIVS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58

```


Db	Qy	Db
255 HAARFKTFWMBSSVYNPEQLASAGFYTVGNSDDVKECCDGGILRMESGSDPEWVQIAK	59 CYPCKKYL 66 : :	314
	315 WPPRCETL 322	

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RESULT 27
US-09-201-936-6
/ Sequence 6, Application US/09201936
/ Publication No. US20020187946A1
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Mackenzie, Alexander E.
/ APPLICANT: Baird, Stephen
/ APPLICANT: Liston, Peter
/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
/ TITLE OF INVENTION: PROBES, AND DETECTION METHODS
/ FILE REFERENCE: 07891/003003
/ CURRENT APPLICATION NUMBER: US/09/201, 936
/ CURRENT FILING DATE: 1998-12-01
/ PRIORITY FILING DATE: 1998-12-01

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? EARLIER FILING DATE: 1998-02-04
? EARLIER APPLICATION NUMBER: PCT/IB96/01022
? EARLIER FILING DATE: 1996-08-05
? EARLIER APPLICATION NUMBER: 08/576,956
? EARLIER FILING DATE: 1995-12-22
? EARLIER APPLICATION NUMBER: 08/511,485
? EARLIER FILING DATE: 1995-08-04
? NUMBER OF SEQ ID NOS: 45
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 6
? LENGTH: 604
? TYPE: PRT
? ORGANISM: Homo sapiens
?S-09-201-936-6

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Query Match	51.3%;	Score 198;	DB 9;	length 604;
Best Local Similarity	55.9%;	Pred. No. 1.7e-15;		
Matches 38;	Conservative	6;	Mismatches 22;	Indels 2;
				Gaps 1

QY 1 YEARI VTPETWIIYS--VNKEQLARAGFYALGSGDKKCFHCGGGLTDWKPSDPRNDQNAK 58
:
Dd 255 HAARFKTFFNWPSSVLTVPQLASAGFYYYGNSDVDVKCFCDGGLCMESGDPPWVQHAK 314

Qy	59	CYPCKXL	66
		: :	
Db	315	WPPRCYL	322

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RESULT 28
US-10-232-286-4
; Sequence 4, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
;
; APPLICANT: Roche, Mike
;
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
;
; NUMBER OF SEQUENCES: 14

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: SOFTWARE: PatentIn Release #1.0, Version #1.30
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/232,286
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? FILING DATE: 30-Aug-2002
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/569,749
?- FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Brezner, David J.
? REGISTRATION NUMBER: 24, 774
? REFERENCE/DOCKET NUMBER: A-62464/DJB
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415)781-1989
? TELEFAX: (415)398-3249
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 604 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 4:
? GS-10-232-286-4

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Query Match	51.3%	Score 198;	DB 14;	Length 604;
Best Local Similarity	55.9%	Pred. No. 1.7e-15;		
Matches 38;	Conservative 6;	Mismatches 22;	Indels 2;	Gaps 1

Qy 1 YEARIIVFGTWITS--VNKEQLRAGFVALGEGDKVKKCHCGGGLTDKRSKSDPMDQHAH 58
: || | | | | | | | | | | | | | | : || | | | |
Db 255 HAARFKTFENNPSLSLVNPEQLASAGFYVVGNSDDVKCFCCDDGRLRCWESGDDPWVQHAH 314

QY	59	CYPCCKYL	66
		: :	
Db	315	WPPRCXYL	322

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RESULT 29
US-10-141-618-6
; Sequence 6, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tumor
; FILE REFERENCE: P-LI 5254
; COPYRIGHT: 1987/10/141 618

```

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; CURRENT FILING DATE: 2002-05-07
;
; PRIOR APPLICATION NUMBER: US 60/289,233
;
; PRIOR FILING DATE: 2001-05-07
;
; PRIOR APPLICATION NUMBER: US 60/256 924

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?
? PRIOR APPLICATION NUMBER: US 09/388,221
? PRIOR FILING DATE: 1999-09-01
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 6
? LENGTH: 604
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-141-618-6

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Query Match	51.35	Score 198	DB 14	Length 604
Best Local Similarity	55.94	Pred. No. 1.7e-15		
Matches 38; Conservative	6	Mismatches 22	Indels 2	Gaps 1

Db 255 HAARFKTFENNPSSVLNPEGLASAGFYVGNDDYKFCDCDGLRCMESGDDPEVQNAK 314

315 WPPRCXYL 322

RESULT 30
US-10-366-307-6
; Sequence 6, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-307-6

Query Match 51.3%; Score 198; DB 15; Length 604;
Best Local Similarity 55.9%; Pred. No. 1,7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 31
US-10-636-065-221
; Sequence 221, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-636-065-221

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1,7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 32

US-10-600-272-6
; Sequence 6, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-6

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1,7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 33
US-10-730-476A-79
; Sequence 79, Application US/10730476A
; Publication No. US20040171105A1
; GENERAL INFORMATION:
; APPLICANT: Du, Chunying
; APPLICANT: Yang, Qiheng
; TITLE OF INVENTION: Method and Composition for Cleaving IAPs
; FILE REFERENCE: 40716(IP-022)
; CURRENT APPLICATION NUMBER: US/10/730,476A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 79
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-730-476A-79

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1,7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 34
US-10-825-282-40
; Sequence 40, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-40

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKSEDPMDQAK 58
Db 255 HAARFRTFFNWPSSVLVNPQLASAGFYVGNSDVXCFCCDGLRCWESGDDPMVOHAK 314
Qy 59 CYPGCKYL 66
Db 315 WFPRCETL 322

RESULT 35
US-10-934-717-4
; Sequence 4, Application US/10934717
; Publication No. US20050037416A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/934,717
; FILING DATE: 03-Sep-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286
; FILING DATE: 30-Aug-2002
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-934-717-4

Query Match 51.3%; Score 198; DB 17; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKSEDPMDQAK 58
Db 255 HAARFRTFFNWPSSVLVNPQLASAGFYVGNSDVXCFCCDGLRCWESGDDPMVOHAK 314
Qy 59 CYPGCKYL 66
Db 315 WFPRCETL 322

RESULT 36
US-10-353-461-8
; Sequence 8, Application US/10353461
; Publication No. US20030176682A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Internuiversitair Instituut voor Biotechnol
; TITLE OF INVENTION: Molecular characterisation of chromosome translocation
; TITLE OF INVENTION: c(11;18) (q21;q21) and its correlation to
; FILE REFERENCE: PMA/MALT/V043
; CURRENT APPLICATION NUMBER: US/10/353,461
; CURRENT FILING DATE: 2003-01-26
; PRIOR APPLICATION NUMBER: US/09/579,692
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/138,834
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-461-8

Query Match 51.3%; Score 198; DB 14; Length 1140;
Best Local Similarity 55.9%; Pred. No. 3.3e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKSEDPMDQAK 58
Db 255 HAARFRTFFNWPSSVLVNPQLASAGFYVGNSDVXCFCCDGLRCWESGDDPMVOHAK 314
Qy 59 CYPGCKYL 66
Db 315 WFPRCETL 322

RESULT 37
US-09-201-936-28
; Sequence 28, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Kornelink, Robert G.

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzlia pseudotsugata
; US-09-201-936-28

Query Match          49.2%; Score 190; DB 9; Length 68;
Best Local Similarity 48.5%; Pred. No. 1.6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;
```

```

QY 3 ARIVTGTWTVSVNK--EQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 3 ARRTFAEMPRGLKQRPBELAEGFFYTGQDXTKRCFCDDGGLKDWEPDAPMOQHARWY 62

QY 61 PGCKYL 66
DB 63 DRCEYV 68

RESULT 38
US-10-041-859-18
; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzlia pseudotsugata
; US-10-041-859-18

Query Match          49.2%; Score 190; DB 14; Length 68;
Best Local Similarity 48.5%; Pred. No. 1.6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;
```

```

QY 3 ARIVTGTWTVSVNK--EQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 3 ARRTFAEMPRGLKQRPBELAEGFFYTGQDXTKRCFCDDGGLKDWEPDAPMOQHARWY 62

QY 61 PGCKYL 66
DB 63 DRCEYV 68
```

```

RESULT 39
US-10-600-272-28
; Sequence 28, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzlia pseudotsugata
; US-10-600-272-28

Query Match          49.2%; Score 190; DB 16; Length 68;
Best Local Similarity 48.5%; Pred. No. 1.6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;
```

```

QY 3 ARIVTGTWTVSVNK--EQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 3 ARRTFAEMPRGLKQRPBELAEGFFYTGQDXTKRCFCDDGGLKDWEPDAPMOQHARWY 62

QY 61 PGCKYL 66
DB 63 DRCEYV 68

RESULT 40
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryzlia pseudotsugata
; US-10-041-859-12

Query Match          49.2%; Score 190; DB 14; Length 172;
Best Local Similarity 48.5%; Pred. No. 4.2e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;
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QY 3 ARIVTGTWTVSVNK--EQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
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Db	70	ARLRTFAEWPRGLKQRPBELAEGFYTGGDKTRCFCDCGILKDWEPDAPMOQHARWY	129
Qy	61	PGCKYL	66
Db	130	DRCEYV	135

Search completed: June 15, 2005, 17:58:16
Job time : 110.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 15, 2005, 17:27:02 ; Search time 23.5 Seconds
(without alignments)
270.226 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYTFGTWIVSVNKEQL.....KPSDPWDHAKYCGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	366	94.8	497	2	S69544	apoptosis inhibitor
2	198	51.3	604	2	S68449	apoptosis inhibitor
3	196	50.8	358	2	UCS964	apoptosis inhibitor
4	190	49.2	268	2	T10304	inhibitor of apopt
5	190	49.2	268	2	A53989	apoptosis-inhibiti
6	184	47.7	618	2	S68450	apoptosis inhibitor
7	177	45.9	298	2	UC7568	kidney inhibitor o
8	175	45.3	275	2	A45679	inhibitor-of-apopt
9	164.5	42.6	1232	2	A55478	neuronal apoptosis
10	160.5	41.6	1447	2	T42628	apoptosis inhibitor
11	149	38.6	496	2	S68452	apoptosis inhibitor
12	149	38.6	497	2	S69545	apoptosis inhibitor
13	141	36.5	208	2	T03183	probable apoptosis
14	128	33.2	275	2	T10310	apoptosis-inhibiti
15	126	32.6	150	2	T28409	ORF MSV248 probabl
16	114.5	29.7	4845	2	T31067	BIR repeat contain
17	108	28.0	286	2	D36828	orf13 protein - Au
18	106	27.5	292	2	T41772	IAP1 orf27 - Bomby
19	100	25.9	155	2	T37471	apoptosis inhibitor
20	99	25.6	155	2	T30469	apoptosis inhibitor
21	93	24.1	308	2	T37474	apoptosis inhibitor
22	84.5	21.9	997	2	T43523	cut17 protein - fi
23	83.5	21.6	329	2	T28403	ORF MSV242 probabl
24	80.5	20.9	564	2	C42523	A55R protein - vac
25	80.5	20.9	564	2	J01792	Salp17R protein -
26	66.5	17.2	187	2	T50621	hypothetical prote
27	66	17.1	511	2	T33634	nicotinic acetylch
28	66	17.1	534	2	T25720	hypothetical prote
29	65.5	17.0	737	2	PQ0219	RNA-2 polypeptide

30	65	16.8	466	2	PC4296	nicotinic acetylch
31	64.5	16.7	334	2	S39502	vegetative storage
32	64.5	16.7	506	2	S13720	coat protein - ara
33	64	16.6	204	2	H70609	probable dna-3-met
34	63	16.3	249	2	H72858	apoptosis inhibito
35	62.5	16.2	336	2	H81785	conserved hypochet
36	61.5	15.9	336	2	H81210	conserved hypochet
37	61.5	15.9	1808	2	T15099	hypothetical prote
38	60.5	15.7	437	2	AG0766	probable dehydrata
39	60.5	15.7	788	2	S70079	1,4-alpha-glucan b
40	60.5	15.7	1798	2	S53869	laminin beta-2 cha
41	60	15.5	246	2	I50127	MHC class II histo
42	60	15.5	249	2	T41814	IAP2 orf71 - Bomby
43	60	15.5	252	2	I50126	MHC class II histo
44	59.5	15.4	459	2	S76138	hypothetical prote
45	59.5	15.4	607	2	T39823	hypothetical prote

ALIGNMENTS

RESULT 1
S69544
apoptosis inhibitor IAP homolog - human
C/Species: Homo sapiens (man)
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S69544; S68451
R/Duckett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C
EMBO J. 15, 2685-2694, 1996
A/Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A/Reference number: S69544; MUID:96256286; PMID:8554366
A/Accession: S69544
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-497 <DUC>
A/Cross-references: UNIPROT:P98170; EMBL:U32974; NID:G1016687; PID:ACS0518.1; PID:G101
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A/Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A/Reference number: A58182; MUID:96149249; PMID:8552191
A/Accession: S68451
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A/Cross-references: EMBL:U45880; NID:G184319; PID:AA050373.1; PID:G1184320
C/Genetics:
A/Gene: IIP
C/Function:
A/Description: apoptotic suppressor
C/Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C/Keywords: Apoptosis; zinc finger
F/446-490/Domain: RING finger homology <RRN>

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. NO. 2e-33;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYTFGTWIVSVNKEQLAPAGFYALGSGDKVCKFCGCGGLTDKPSDPWDHAKY 60
DB 265 YEARIYTFGTWIVSVNKEQLAPAGFYALGSGDKVCKFCGCGGLTDKPSDPWDHAKY 324

OY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 2
S68449
apoptosis inhibitor hiap-1 - human
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: S68449
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,

Nature 379, 343-353, 1996

ARTitle: Suppression of apoptosis in mammalian cells by NALP and a related family of IAP

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68449

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-604 <LIS>

A:Cross-references: UNIPROT:Q13489; EMBL:U45678; NID:g1184315; PIDN:AACS0371.1; PID:g1184315

A:Description: apoptotic suppressor

C:Keywords: apoptosis; zinc finger

F:553-597/Domain: RING finger homology <RNG>

C:Function:

Query Match 51.3%; Score 198; DB 2; Length 604;

Best Local Similarity 55.9%; Pred. No. 1.8e-14;

Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIIVFGTIVY--VNKEQLARAGFYALGEGDKVKCFHCGGLITMVKSEDPWDQNAK 58

DB 255 HAARKTITFNNPSSVLPVNPPEQLASGFTYVGNSDVVKFCDCDGLRCWESGDPEWQNAK 314

QY 59 CYPGCKYL 66

DB 315 WFPRCXYL 322

RESULT 3

JCS964

apoptosis inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C:Accession: JCS964

R:Steinlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.

A:Title: Cyclokin induced expression of porcine inhibitor of apoptosis protein (IAP) fam

A:Reference number: JCS964; MUID:98162622; PMID:9501011

A:Accession: JCS964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: UNIPROT:O62640; GB:U79142; NID:g29572174; PIDN:AAC39171.1; PID:g29572174

F:307-351/Domain: RING finger homology <RRN>

Query Match 50.8%; Score 196; DB 2; Length 358;

Best Local Similarity 54.4%; Pred. No. 1.9e-14;

Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIIVFGTIVY--VNKEQLARAGFYALGEGDKVKCFHCGGLITMVKSEDPWDQNAK 58

DB 90 YAAAFKTFKCNPPSIPVHPPEQLASGFTYVGNHSDVVKFCDCDGLRCWESGDPEWQNAK 149

QY 59 CYPGCKYL 66

DB 150 WFPRCXYL 157

RESULT 4

T10304

inhibitor of apoptosis protein 3 - Orygia pseudotangata nuclear polyhedrosis virus

C:Species: Orygia pseudotangata nuclear polyhedrosis virus, OpMPV

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000

C:Accession: T10304

R:Altrens, C.A.; Ruseell, R.R.; Funk, C.U.; Evans, J.; Hatwood, S.; Rohrmann, G.F.

A:Title: The sequence of the Orygia pseudotangata multinucleocapsid nuclear polyhedrosis

A:Reference number: Z17011; MUID:97271300; PMID:9126251

A:Accession: T10304

A:Status: preliminary; translated from GB/EMBL/DBDUT

A:Molecule type: DNA

A:Residues: 1-268 <AIR>

A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AACS034.1; PID:g1911281

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology <RRN>

Query Match	49.2%	Score 190	DB 2	Length 268
Best Local Similarity	48.5%	Pred. No. 6,7e-14		
Matches	32	Conservative 12	Mismatches 20	Indels 2
<p>Gaps 1</p>				
<p>Query Match</p>				
<p>Best Local Similarity</p>				
<p>Matches</p>				
<p>Gaps</p>				
<p>Query Match</p>				
<p>Best Local Similarity</p>				
<p>Matches</p>				
<p>Gaps</p>				
<p>Query Match</p>				
<p>Best Local Similarity</p>				
<p>Matches</p>				
<p>Gaps</p>				
<p>Query Match</p>				
<p>Best Local Similarity</p>				
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<p>Gaps</p>				
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<p>Best Local Similarity</p>				
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<p>Query Match</p>				
<p>Best Local Similarity</p>				
<p>Matches</p>				
<p>Gaps</p>				
<p></p>				


```

OY      1 YEARIIVTGTWY-----SVNKEQLAAGFALALGEGKVKCFHCGGGLTWMKSEDPWD 54
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      17 YKRLMTKRNFEYDDBDPACKTSQAVQAAGFYCTGP--OSGKCAFCNNKL--DFDPEDWY 74

OY      55 QHAKCYPCCKYL 66
      : | | : : :
DB      75 EHTKDEPCFCFY 86

RESULT 20
T30489
apoptosis inhibitor - lymphantria dispar nuclear polyhedrosis virus
C:Species: Lymphantria dispar nuclear polyhedrosis virus, LdMNPV
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30489
R:Kusio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohd
V:Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymphantria
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30489
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-155 <KUZ>
A:Cross-references: UNIPROT:Q9YMI9; EMBL:AF081810; PIDD:AAC70325.1

Query Match
Best Local Similarity 25.6%; Score 99; DB 2; Length 155;
Matches 19; Conservative 12; Mismatches 32; Indels 2; Gaps 1;

OY      4 RIVFTGTW--IYSVNKEQLAAGFALGEGKVKCFHCGGGLTWMKSEDPWDQHAKCYP 61
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      7 RLASFRRNSAVDAPAPAPALAHAGFYCANRQDFVCAYCHIEIGMWSIGSDMSHKKYSP 66

OY      62 GCKTL 66
      : : :
DB      67 ACRFY 71

RESULT 21
T37474
apoptosis inhibitor homolog C50B8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37474; T20098
R:Uren, A.G.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z21711
A:Accession: T37474
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308 <URE>
A:Cross-references: UNIPROT:Q18727; EMBL:U72208; PIDD:AAD00182.1
R:Petcy, C.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19223
A:Accession: T20098
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-308 <WIL>
A:Cross-references: EMBL:Z77654; PIDD:CA01130.1; GSPDB:GN00023; CESP:C50B8.2
C:Genetic8:
A:Experimental source: clone C50B8
A:Gene: C50B8.2
A:Map position: 5
A:Introns: 48/3; 143/1; 191/3

Query Match
Best Local Similarity 24.1%; Score 93; DB 2; Length 308;
Matches 22; Conservative 20; Mismatches 23; Indels 10; Gaps 4;

OY      1 YEARIIVTGTWYSVNK-----EQIARAGFYAL--GEGDK--VVCFFCGGGLTWMKSESD 51
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      167  FDRRLATFQNFIFDDKGRNVKCTISKLLAKGWFSTIAKKDXTSAKCPCLVEL-DFDESDD 225
QY      52  PWDQAKCYPGCKYL 66
      ||::||::||
Db      226  PWEHQKFSASCDPI 240

RESULT 22
T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43523; T41649; T41700
R:Morishita, J.; Matsusaka, T.; Yanagida, M.
Submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cut17 is required for chromosome segregation.
A:Reference number: Z22536
A:Accession: T43523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <MOR>
A:Cross-references: UNIPROT:O14064; EMBL:AB031034; PIDN:BAAB3415.1
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, August 1998
A:Reference number: Z22007
A:Accession: T41649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <HAR>
A:Cross-references: EMBL:AL013123; PIDN:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02C
R:Experimental source: strain 972h; cosmid c362
R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, October 1999
A:Reference number: Z22010
A:Accession: T41700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 932-997 <MED>
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10C
C:Genetics:
A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10C
A:Map position: 3L
A:Introns: 43/3

Query Match      21.9%; Score 84.5; DB 2; Length 997;
Best Local Similarity 30.3%; Pred. No. 0.17;
Matches 23; Conservative 8; Mismatches 34; Indels 11; Gaps 3;

QY      1  YEARIYVFGTWIYSVNK--EQLARAGFY--ALGEG-----DKVCFHCGGGITDWKPS 49
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      22  YSKRLDTFOKKMKPRAKFPETLATGVFYNNPISSENSSEBRLDNTVTCYMTKSFYDWEED 81
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
QY      50  EDPWDQAKCYPGCKY 65
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      82  DDPLKEHTTSPSCPW 97
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 23
T28403
ORF MSV442 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomop
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28403
R:Afonso, C.L.; Tulman, B.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28403
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-329 <AFO>
A:Cross-references: UNIPROT:O9YVK0; EMBL:AF063866; NID:94049647; PIDN:AAC97721.1; PID:94(4
C:Genetics:

```


RESULT 28
T25720
hypothetical protein F21F3.5 - *Caenorhabditis elegans*
C|Species: *Caenorhabditis elegans*
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C|Accession: T25720
R|Geisel, C.; Kramer, J.; Elliott, G.
submitted to the EMBL Data Library, February 1997
A|Description: The sequence of *C. elegans* cosmid F21F3.
A|Reference number: Z20075
A|Accession: T25720
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-534 <GRI>
A|Cross-references: EMBL,U081175; PIDN:AAB42282.1; GSPDB:GN00019; CESP:F21F3.5
A|Experimental source: strain Bristol N2; clone F21F3
C|Genetics:
A|Gene: CESP:F21F3.5
A|Map position: 1
A|Intons: 43/2; 66/3; 118/2; 168/3; 248/3; 271/3; 364/1; 507/3
A|Superfamily: acetylcholine receptor

[illegible]

RESULT 29
PQ0219 RNA-2 polyprotein - arabis mosaic virus (fragment)
N/Contains: coat protein
C/Species: arabis mosaic virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: PQ0219; PQ0220
R/Bertolotti, D.J.; Harris, R.D.; Edwards, M.L.; Cooper, J.I.; Hawes, W.S.
J. Gen. Virol. 72, 1801-1809, 1991
A/Title: Transgenic plants and insect cells expressing the coat protein of arabis mosaic
A/Reference number: PQ0219; MUID:91341466; PMID:1875193
A/Accession: PQ0219
A/Molecule type: genomic RNA
A/Residues: 1-737 <BER>
A/Cross-references: UNIPROT:Q65028; GB:DJ0086; NID:g221017; PIDN:BA00982.1; PID:di00145
A/Experimental source: strain lilac
A/Accession: PQ0220
A/Molecule type: protein
A/Residues: 233-252 <BE2>
C/Genetics:
A/Map position: segment RNA-2
C/Keywords: polyprotein
C/233-737/Product: coat protein #status experimental <COA>

Query Match	17.0%	Score 65.5;	DB 2;	Length 737;
Best Local Similarity	32.3%;	Pred. No. 17;		
Matches 20; Conservative	8;	Mismatches 19;	Indels 15;	Gaps 4

Qy 12 IYSVNNEOLARAGFALGSDKVK-----CFHCGGL-----TDWKSEEDPWQHACYP 61
:
:
:
Db 447 VINFNNTLIS----YLLIGGVKKGMHICSPCTTGIVLRVSVEMGNVTNNMQLFX-YP 501
:
:
:
Qy 62 GC 63
:
:
b 502 GC 503

RESULT 30
 PC4236
 nicotinic acetylcholine receptor alpha chain - nematode (*Trichostrongylus colubriformis*)
 N:Alternate names: tar-1 protein
 C:Species: *Trichostrongylus colubriformis*
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C:Accession: PC4236
 R:Wiley, L.J.; Weiss, A.S.; Sangster, N.C.; Li, Q.
 Gene 182, 97-100, 1996
 A>Title: Cloning and sequence analysis of the candidate nicotinic acetylcholine receptor
 A:Reference number: PC4236; MUID:9713696; PMID:8962073
 A:Accession: PC4236
 A:Molecule type: DNA
 A:Residues: 1-466 <MIL>
 A:Cross-references: UNIPROT:Q94789; GB:U56903
 C:Genetics:
 A:Gene: tar-1
 C:Superfamily: acetylcholine receptor
 F:214-239/Domain: transmembrane #status predicted <TM1>
 F:247-270/Domain: transmembrane #status predicted <TM2>
 F:276-289/Domain: transmembrane #status predicted <TM3>
 F:415-436/Domain: transmembrane #status predicted <TM4>

```

Query Match      16.8% Score 65; DB 2; Length 466;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 20; Conservative 11; Mismatches 19; Indels 26; Gaps 4.

QY      8 FGTITVTVN-----KEQLARAGFYALAGEGDKVCFCFGCGGLTMMKPSDEPMD 54
          ||| | | | | | : | : | : | : | : | : | : | : | : | : |
Db       126 FGSMVTSSNLINLLENNARYEEIEINSGVV-----DNITIADEGIDLSDYPSFVE-WD 179
          ||| | | | | | | | | | | | | | | | | | | | | | | |

QY      55 -----QHAKCYPGC 63
          : | : | | | | | | | | | | | | | | | | | | | | | | |
Db       180 IMSRVARRRSKNYPSC 195
          : | : | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 31
S39502
Vegetative storage protein win4.5 - western balsam poplar x cottonwood (fragment)
C:Species: Populus trichocarpa x Populus deltoides (western balsam poplar x cottonwood)
C:Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S39502
R:David, J.M.; Egglekrout, E.B.; Coleman, G.D.; Chen, T.H.H.; Haissig, B.E.; Riemschneidt
Plant Mol. Biol. 23, 135-143, 1993
A:Title: A family of wound-induced genes in Populus shares common features with genes enc
A:Reference number: S39502; MUID:94033285; PMID:8106009
A:Accession: S39502
A:Molecule type: mRNA
A:Residues: 1524 <DNA>
A:Cross-references: UNIPROT:O41097; EMBL:L20233; NID:G309838; PTD:G309839

Query Match      16.7%  Score 64.5  DB 2  Length 324  ;
Best Local Similarity 32.8%  Pred. No. 10  ;
Matches 22; Conservative 4; Mismatches 24; Indels 17; Gaps 3;

```

[illegible]

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RESULT 32
S13720
coat protein - arabis mosaic virus (fragment)
C/Dspecies: arabis mosaic virus
C/Ddate: 13-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S13720; S77995
R:/Steinkellner, H.; Himmelr, G.; Maltanovich, D.; Kallinger, H.
Nucleic Acids Res. 18, 7182, 1990

```

A>Title: Nucleotide sequence of AMV-capsid protein-gene.
A/Reference number: S13720; MUID:91088343; PMID:2263501
A/Accession: S13720
A/Molecule type: genomic RNA
A/Residues: 1-506 <STE>
A/Cross-references: UNIPROT:P24819; EMBL:X55460
A/Accession: S77995
A/Molecule type: protein
A/Residues: 2-21 <HM>
A/Keywords: polypeptide
P:2-506/Product: coat protein #status predicted <COA>

Query Match 16.7%; Score 64.5; DB 2; Length 506;
Best Local Similarity 32.3%; Pred. No. 16;
Matches 20; Conservative 8; Mismatches 19; Indels 15; Gaps 4;

Qy 12 IYSNKGQARAGYALGEGDKV-----CFHCGGL-----TWKSESDPMDQAKCYR 61
Db 216 VYNNNTLLS---YYIGIGIVKGVKRVCSPTGYIVLRVSBMNGVTNNQLFK-YP 270
|||
Qy 62 GC 63
|||
Db 271 GC 272

RESULT 33

H70609

probable dna-3-methyladenine glycosylase I - Mycobacterium tuberculosis (strain H37Rv)

C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: H70609

R/Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rastandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Square, S.
Nature 393, 537-544, 1998

A/Authors: Sgarbes, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: H70609

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-204 <COL>

A/Cross-references: UNIPROT:O05311; GB:Z93777; GB:AL123456; NID:G3261726; PIDN:CAB07833

A/Experimental source: strain H37Rv

C/Genetics:

A/Gene: tagA

C/Superfamily: 3-methyladenine DNA glycosylase I

Query Match 16.6%; Score 64; DB 2; Length 204;
Best Local Similarity 31.8%; Pred. No. 7.5;
Matches 21; Conservative 7; Mismatches 22; Indels 16; Gaps 3;

Qy 9 GTWYYSNKE-----QLARAGYALGEGDKVCFHCGGLTD-----WKPSEDPMDQHA 57
|||
Db 139 GSELPSTSTSKAMSRKRGFRFVPTTAYALMQRATGMVDHIOACWPTERPFDQ-- 196
|||

Qy 58 KCVPGC 63
|||
Db 197 ---PGC 199

RESULT 34

H72858

apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus

C/Species: Autographa californica nuclear polyhedrosis virus, AcMNPV

A/Note: dbDNA virus

C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C/Accession: H72858

R/Artes, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A/Reference number: A72850; MUID:94303173; PMID:8030224

A/Accession: H72858

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <AYR>
A/Cross-references: UNIPROT:P41454; GB:U22858; NID:G510708; PIDN:AAA66701.1; PID:G559140
A/Genes: Ac-IAP2

Query Match 16.3%; Score 63; DB 2; Length 249;
Best Local Similarity 32.1%; Pred. No. 12;
Matches 17; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

Qy 14 SVNKGQARAGYALGEGDKVCFHCGGLTWKSESDPMDQAKCYRPGCKYL 66
Db 103 SVVVDMLARGFYFGKAGHRCSCG-HVFKYKSYDDAQRHKKQ--NCKFL 151
|||

RESULT 35

H81785

conserved hypothetical protein NMA2139 [imported] - Neisseria meningitidis (strain Z2491

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: H81785

R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rastandream, Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: H81785

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-336 <PAR>

A/Cross-references: UNIPROT:Q9JST9; GB:AL162758; GB:AL157959; NID:G7380672; PIDN:CAB85353

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA2139

C/Superfamily: Haemophilus influenzae conserved hypothetical protein HI0634

Query Match 16.2%; Score 62.5; DB 2; Length 336;
Best Local Similarity 30.6%; Pred. No. 18;
Matches 19; Conservative 7; Mismatches 17; Indels 19; Gaps 3;

Qy 1 YEARIYFTGWTIYSVNKEQARAGYALGEGDKVCFHCG-----GGLTWKPSEDP 52
|||
Db 28 YMARQITRNTWLYS---EWVNAGAIYVGDKRFLEMEGEGPVALQLG-----SDP 76
|||

Qy 53 WD 54
|||
Db 77 SD 78

RESULT 36

B81210

conserved hypothetical protein NMB0348 [imported] - Neisseria meningitidis (strain MC58

C/Species: Neisseria meningitidis

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: B81210

R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A/Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: B81210

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-336 <TET>

A/Cross-references: UNIPROT:Q9K142; GB:AB002391; GB:AB002098; NID:G7225561; PIDN:AAF40793

A/Experimental source: serogroup B, strain MC58

C/Genetics:

A/Gene: NMB0348

C/Superfamily: Haemophilus influenzae conserved hypothetical protein HI0634


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Query Match      15.9%; Score 61.5; DB 2; Length 336;
Best Local Similarity 30.6%; Pred. No. 23;
Matches 19; Conservative 7; Mismatches 17; Indels 19; Gaps 3;

OY      1 YEARIVFGTWIVSVNKEQLARAGFYALGEGDVKYKCHCG-----GGITDWRKPSDDP 52
Db      28 YLARIQTRNTWLVIS-----EMVNAQAIYVGDKDRFLMFEQGPVALQLQGG-----SDP 76

OY      53 WD 54
Db      77 SD 78

RESULT 37
T15099
hypothetical protein W03F8.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15099
R/Johnson, D.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03F8.
A/Reference number: Z18293
A/Accession: T15099
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1808 <JOH>
A/Cross-references: UNIPROT:O44565; EMBL:AF039041; NID:g2736380; PID:g2736388; PIDN:AB39
C/Genetics:
A:Gene: CBSP:W03F8.5
A:Map position: 4
A/Intons: 99/2; 255/2; 365/2; 435/3; 565/2; 975/2; 1055/2; 1602/3; 1719/3; 1766/1
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
F/797-842/Domain: laminin-type EGF-like homology <LEG>

Query Match      15.9%; Score 61.5; DB 2; Length 1808;
Best Local Similarity 40.9%; Pred. No. 1.2e+02;
Matches 9; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

OY      32 DKVCFHCGGGLTDMKPSDDPW 53
Db      74 EQTKCFYC-DSRTMKPQREPY 94

RESULT 38
AG0766
probable dehydratase RfBH rfBH [imported] - Salmonella enterica subsp. enterica serovar
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0766
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Crofton, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moutle, S.; O'Geare, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AG0766
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-437 <PAR>
A/Cross-references: GB:AL513383; PIDN:CAD02453.1; PID:G16503320; GSPDB:GN00176
C/Genetics:
A:Gene: rfBH
C:superfamily: erythromycin resistance protein

Query Match      15.7%; Score 60.5; DB 2; Length 437;
Best Local Similarity 31.9%; Pred. No. 39;
Matches 22; Conservative 4; Mismatches 26; Indels 17; Gaps 4;

OY      1 YEARIV-TFGTWIVSVNKEQLARAGFY-----ALGSDGVKCFHCGGGLTDMKPSDDPW 54

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Db      200 YEGRMVGTFG-----DIGTSFYPAHHTITBEGAV--FTKSGELKTIIESPRDWG 248

OY      55 QHAKCYPGC 63
Db      249 RDCYCAPGC 257

RESULT 39
S70079
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I - Streptomyces coelicolor
N/Alternate names: glycogen branching enzyme
C/Species: Streptomyces coelicolor
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S70079; T42040
R/Brunon, C.U.; Plaakite, K.A.; Chater, K.F.
Mol. Microbiol. 18, 89-99, 1995
A/Title: Tissue-specific glycogen branching isoenzymes in a multicellular prokaryote, Str
A/Reference number: S70078; MUID:96154943; PMID:8596463
A/Accession: S70079
A/Molecule type: DNA
A/Residues: 1-788 <BRU>
A/Cross-references: UNIPROT:O59833; EMBL:X83397; NID:g1061285; PIDN:CA58314.1; PID:g1061
A/Experimental source: strain A3(2)
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
A/Note: only a part of the nucleic acid sequence is shown
A/Note: only a part of the translation is shown
C/Genetics:
A:Gene: glgBI
A:Start codon: GNG
C/Superfamily: 1,4-alpha-glucan branching enzyme
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match      15.7%; Score 60.5; DB 2; Length 788;
Best Local Similarity 35.6%; Pred. No. 68;
Matches 21; Conservative 3; Mismatches 18; Indels 17; Gaps 4;

OY      9 GTWIVSVNKEQLARAGFYA-----LGEGRVK-----CFHCG-GGLTDMKPSDDPWQHA 57
Db      348 GSWGYGV-----TSFYAPTRALGDPDDFKYLVDRHRAIGVILMDWVPAHFPRDWA 399

RESULT 40
S53869
laminin beta-2 chain precursor (version 2) - human
N/Alternate names: s-laminin
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C/Accession: S53869
R/Itivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggv
Matrux Biol. 14, 489-497, 1994
A/Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss
A/Reference number: S53869
A/Accession: S53869
A/Molecule type: mRNA
A/Residues: 1-1798 <ITV>
A/Cross-references: UNIPROT:P55268
C/Genetics:
A:Gene: GDB:LAMB2
A/Cross-references: GDB:132363; OMIM:150325
A/Map position: 3p21.3-3p21.2
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C/Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F/1-32/Domain: signal sequence #status predicted <SIG>
F/33-1798/Product: laminin beta-2 chain #status predicted <MAT>
F/283-344/Domain: laminin-type EGF-like homology <LEB1>
F/347-407/Domain: laminin-type EGF-like homology <LEB2>
F/410-467/Domain: laminin-type EGF-like homology <LEB3>
F/470-519/Domain: laminin-type EGF-like homology <LEB4>
F/522-552/Domain: laminin-type EGF-like homology #status atypical <LEB5>
F/783-828/Domain: laminin-type EGF-like homology <LEB6>
F/831-874/Domain: laminin-type EGF-like homology <LEB7>
F/877-924/Domain: laminin-type EGF-like homology <LEB8>

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F;927-983/Domain: laminin-type EGF-like homology <LE09>
F;986-1035/Domain: laminin-type EGF-like homology <LE10>
F;1038-1092/Domain: laminin-type EGF-like homology <LE11>
F;1095-1140/Domain: laminin-type EGF-like homology <LE12>
F;1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 15.7%; Score 60.5; DB 2; Length 1798;
Best local Similarity 32.7%; Pred. No. 1.5e+02;
Matches 16; Conservative 5; Mismatches 25; Indels 3; Gaps 2;

OY 19 QLARAGFVALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHA-KCYPGCKYL 66
DB 450 QQCRDGFPGLSISDRLGCRRCQCNARGTVPGSTPCDPNPGSGCY--CKRL 496

Search completed: June 15, 2005, 17:40:28
Job time : 25.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:19:12 ; Search time 112.5 Seconds

(without alignments)
300.420 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYFTGWTIVSYVNKEQL.....KPSDPWDQHAKYPCGCKYL 66

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprotc:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	94.8	496	1 BIR4 RAT	Q9R016 ratu
2	366	94.8	496	2 Q9ESF0	Q9ESF0 ratu
3	366	94.8	497	1 BIR4 HUMAN	P98170 homo
4	366	94.8	501	2 Q9EQD4	Q9EQD4 ratu
5	361	93.5	501	2 Q9EQD5	Q9EQD5 ratu
6	357	92.5	496	1 BIR4 MOUSE	Q60989 mus
7	334	86.5	236	1 BIR8 HUMAN	Q60989 mus
8	334	86.5	236	2 Q6PIY1	Q6PIY1 homo
9	328	85.0	236	1 BIR8 PANTR	Q9SM72 pan
10	325	84.2	236	1 BIR8 GORGO	Q9SM71 gor
11	306	79.3	106	2 Q9URW6	Q9URW6 homo
12	279	72.3	493	2 Q9URW8	Q9URW8 homo
13	258	66.8	109	2 Q8WMT4	Q8WMT4 gall
14	258	66.8	109	2 Q8WMT4	Q8WMT4 gall
15	212	54.9	322	2 Q8WMT4	Q8WMT4 gall
16	212	54.9	405	2 Q8WMT4	Q8WMT4 gall
17	212	54.9	415	2 Q7SXU1	Q7SXU1 brach
18	204	52.8	280	2 Q6VTY9	Q6VTY9 brach
19	198	51.3	604	1 BIR3 HUMAN	Q13489 homo
20	196	50.8	287	1 Q6E7G7	Q6E7G7 antica
21	196	50.8	358	1 P1AP PIG	Q66640 sus
22	192	49.7	195	2 Q9IA70	Q9IA70 gall
23	192	49.7	197	2 Q9IA69	Q9IA69 gall
24	192	49.7	602	2 Q9ESB9	Q9ESB9 ratu
25	190	49.2	611	1 BIR CHICK	Q90660 gall
26	190	49.2	268	1 IAP3 NPVOP	P41437 ocr
27	189	49.0	269	2 Q6OX76	Q6OX76 agroc
28	189	49.0	374	2 Q921N0	Q921N0 mus
29	189	49.0	600	1 BIR3 MOUSE	Q08863 mus
30	189	49.0	616	2 Q804E2	Q804E2 icta
31	189	49.0	628	2 Q8UWD2	Q8UWD2 brach

32	189	49.0	647	2 Q7T0K2	Q7T0K2 brach
33	189	49.0	654	2 Q6ZM93	Q6ZM93 brach
34	185	47.9	346	2 Q8IS31	Q8IS31 bomby
35	185	47.9	346	2 Q968T8	Q968T8 bomby
36	185	47.9	589	2 Q9ESB8	Q9ESB8 ratu
37	185	47.9	589	2 Q9QZC6	Q9QZC6 ratu
38	184	47.7	589	2 Q6P6S1	Q6P6S1 ratu
39	184	47.7	612	1 BIR2 MOUSE	Q62210 mus
40	183	47.4	534	2 Q81ZD0	Q81ZD0 homo
41	183	47.4	604	2 Q6DDY3	Q6DDY3 xenop
42	183	47.4	618	1 BIR2 HUMAN	Q13490 homo
43	181	46.9	604	2 Q6GLD7	Q6GLD7 xenop
44	180	46.6	263	2 Q80SF4	Q80SF4 hyph
45	180	46.6	283	2 Q80LX8	Q80LX8 adoxo

ALIGNMENTS

RESULT 1
BIR4 RAT
ID BIR4 RAT STANDARD; PRT; 496 AA.
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein) (X-linked IAP)
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP) (RIAP-3).
GN Name=Birc4; Synonyms=Ap13, XIap;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25, these interactions inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRS25 are mediated by the second and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB033366; BAA85304.1; -
CC HSSP; P98170; 1151.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC AP00089; Repeat; Zinc-finger.
CC REPEAT 26 BIR 1.

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FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-type.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 94.8%; Score 366; DB 1; Length 496;
Best Local Similarity 93.9%; Pred. No. 4.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVFTGFWISVNNKQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKCY 60
Db YDARIIVFTGFWISVNNKQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
Q9ESFO PRELIMINARY; PRT; 496 AA.
ID Q9ESFO
AC Q9ESFO;
DT 01-MAR-2001 (TRENBLREL. 16; Created)
DT 01-MAR-2001 (TRENBLREL. 16; Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24; Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes.";
RL BMC Genomics 3:5-5(2002).
DR EMBL; AF183429; AACG22969.1; -.
DR HSP; P98170; I151.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01262; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
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Query Match 94.8%; Score 366; DB 2; Length 496;
Best Local Similarity 93.9%; Pred. No. 4.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVFTGFWISVNNKQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKCY 60
Db YDARIIVFTGFWISVNNKQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
BIR_HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9NQ14;
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
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DT 25-OCT-2004 (Rel. 45; Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP-like protein) (HILP).
GN Name=BIRC4; Synonyms=API3, IAP3, XIAP;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA Gifflian M.C., Shields H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors.";
RL EMO J. 15:2685-2694(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=23188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplinton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pang C.,
RA Baha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Senger A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442; DOI=10.1038/40901;
RA Devereaux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
RL Nature 388:300-304(1997).
RN [6]
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410; DOI=10.1074/jbc.M109891200;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "Ira2 promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins.";
RL J. Biol. Chem. 277:445-454(2002).
RN [7]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637; DOI=10.1038/35050006;
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RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Friis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL: AF304334; AAC41193.1; -.
DR HSSP: P98170; 1151.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FE2E0C8CD CRC64;

Query Match 94.8%; Score 366; DB 2; Length 501;
Best Local Similarity 93.5%; Pred. No. 5e-35; Indels 0; Gaps 0;
Matches 61; Conservative 3; Mismatches 1;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 264 YDARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 5
Q9E005 PRELIMINARY; PRT; 501 AA.
AC Q9E005;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Friis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL: AF304333; AAC41192.1; -.
DR HSSP: P98170; 1151.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56548 MW; 0973F8F28E81C5A0 CRC64;

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Query Match 93.5%; Score 361; DB 2; Length 501;
Best Local Similarity 92.4%; Pred. No. 2e-34;
Matches 61; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 264 YDARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGLADMKPSDPMDOHAKMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
BIR4 MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60985; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN Name=Birc4; Synonyms=A1pa, Api3, Miha, Xiap;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=8643514; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farhant R., Lefebvre C., Korneluk R.G., Mackenzie A.B.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS825; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS825 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U36842; AAC52594.1; -.
DR EMBL: U88990; AAB58376.1; -.
DR HSSP: P98170; 1151.
DR MGD; MGI:107572; Birc4.
DR GO: GO:0001719; P:inhibition of caspase activation; IDA.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.

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DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS00143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Apoptosis; Repeat; Zinc-finger.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT ZN_FING 264 329 BIR 3.
FT CONFLICT 449 484 RING-type.
FT CONFLICT 208 208 RING-type.
FT CONFLICT 317 317 E -> K (in Ref. 2).
FT CONFLICT 322 322 W -> C (in Ref. 2).
FT CONFLICT 346 346 S -> P (in Ref. 2).
FT CONFLICT 360 360 I -> L (in Ref. 2).
FT CONFLICT 388 388 C -> S (in Ref. 2).
FT CONFLICT 449 449 V -> F (in Ref. 2).
FT CONFLICT 462 462 V -> A (in Ref. 2).
FT CONFLICT 468 468 K -> N (in Ref. 2).
FT CONFLICT 490 490
SQ SEQUENCE 496 AA; 56079 MW; ECSFAB0799F2CDD8 CRC64;

Query Match 92.5%; Score 357; DB 1; Length 496;
Best Local Similarity 93.9%; Pred. No. 5.8e-34;
Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YEARIYFGTWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQDAKCY 60
Db 264 YEARIYFGTWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQDAKCY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
BIR_HUMAN
ID BIR_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (inhibitor of apoptosis-
  like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
  inhibitor of apoptosis).
GN Name=BIRC8; Synonyms=ILP2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143; DOI=10.1006/geno.2001.6635;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Mator J.,
RA Rajcan-Separovic B., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
  identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richer B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Pratiati A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Nottarangelo L.D., Vezoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
  apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX.
CC -1- SUBUNIT: Binds to caspase-9.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC -1- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -1- SIMILARITY: Belongs to the IAP family.

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CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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  or send an email to license@isb-sib.ch).
-----
CC EMBL; AF420440; AAL30369.1; -.
CC EMBL; AF164682; AAK81892.1; -.
CC HSSP; P98170; 1G73.
CC Genew; HGNC:14878; BIRC8.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_fing.
CC Pfam; PF00653; BIR; 1.
CC SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS00143; BIR_REPEAT_2; 1.
DR PROSITE; PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Apoptosis; Zinc-finger.
FT REPEAT 7 70 BIR.
FT ZN_FING 189 224 RING-type.
FT CONFLICT 196 196 Y -> H (in Ref. 2).
SQ SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFA9D CRC64;

Query Match 86.5%; Score 334; DB 1; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.5e-31;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFGTWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQDAKCY 60
Db 4 YEARIYFGTWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQDAKCY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 8
OSPIAO
ID OSPIAO PRELIMINARY; PRT; 236 AA.
AC OSPIAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Baculoviral IAP repeat-containing 8.
GN Name=BIRC8;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
RA Diatchenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Halton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC039318; ANH39318.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR_1.
DR SMART: SM00238; BIR; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PSS0143; BIR_REPEAT_2; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 236 AA; 27077 MW; DF8350311PDAFBF CRC64;

Query Match 86.5%; Score 334; DB 2; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.5e-31;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWISVVKQELARAGFYALBGGDKYKCFHGGGLTDMKPSBPDMDHAKCY 60
Db 4 YEARIYFTGWISVVKQELARAGFYALBGGDKYKCFHGGGLTDMKPSBPDMDHAKCY 63
Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 9
061PYL
ID 061PYL PRELIMINARY; PRT; 338 AA.
AC 061PYL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE BIRC8 protein.
GN Name=BIRC8;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC071665; ANH71665.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR_2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PSS0143; BIR_REPEAT_2; 2.
DR PROSITE: PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 338 AA; 38622 MW; DC17979CFC92E3ADF CRC64;

Query Match 86.5%; Score 334; DB 2; Length 338;
Best Local Similarity 81.8%; Pred. No. 2.2e-31;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWISVVKQELARAGFYALBGGDKYKCFHGGGLTDMKPSBPDMDHAKCY 60
Db 106 YEARIYFTGWISVVKQELARAGFYALBGGDKYKCFHGGGLTDMKPSBPDMDHAKCY 165
Qy 61 PGCKYL 66
Db 166 PGCKYL 171

RESULT 10
BIR8_PANTR
ID BIR8_PANTR STANDARD; PRT; 236 AA.
AC 095W72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonym=ILP2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1126/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Praticelli A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Verzoni P., Fearnshead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RT Mol. Cell. Biol. 21:4292-4301(2001).
RN [1]
RP FUNCTION: Protects against apoptosis mediated by BAX (by
RP similarity).
CC - SUBUNIT: Binds to caspase-9 (by similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC - SIMILARITY: Belongs to the IAP family.
CC - SIMILARITY: Contains 1 BIR repeat.
CC - SIMILARITY: Contains 1 RING-type zinc finger.
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CC EMBL; AY030052; AAK49776.1; -.
CC -----
DR HSPD, P98170.1G73.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SMO0238; BIR; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR KWT Apoptosis; zinc-finger.
DR REPEAT 70
DR ZN_FING 189 224 BIR.
DR FT 236 AA; 27136 MW; 640CAJA251420EDE CRC64;
DR SO SEQUENCE

Query Match 85.0%; Score 328; DB 1; Length 236;
Best Local Similarity 80.3%; Pred. No. 7,9e-31;
Matches 53; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARIVTFTGTVIYSVKNQOLAPAGFYALGSDKVKCFHCGGGLTDWPKSEDPWDQAKY 60
DB 4 YEALITFGTWMVYFVNKEQLARAGFYAIGEDKVKCFHCGGGLANWPKEDPMDQAKY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 11
BIR8.GORGO STANDARD; PRT; 236 AA.
AC Q95M71;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonyms=ILP2;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Raffey S.B.,
RA Fratini A., Tlan L., Frank S., Youle R.J., Nelson D.L.,
RA Nocarangelo L.D., Vezzoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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Query Match	326	DB 1	length 236
Best Local Similarity	80.3%	Pred. No.	7.9e-31
Matches	53	Conservative	8
		Mismatches	5
		Indels	0
		Gaps	0

[illegible]

QY	61	PGCKYL	66
Db	64	PGCKYL	69

Db 64 PGCKYL 69

	RESULT 11
BIR8_GORGO	ID
_BIR8_GORGO	STANDARD;
Q95M71;	PRT; 236 AA.
DT 28-FEB-2003 (Rel. 41, Created)	
DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DE Bacterial IAP repeat-containing protein 8 (Inhibitor of apoptosis-like protein 2) (IAP-like protein 2) (ILP-2).	
GN Name=BIRC8, Synonyms=ILP2;	
OS Gorilla gorilla gorilla (Lowland gorilla).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.	
OX NCBI_Taxid=9595;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21286921; PubMed=11390657;	
RA DOI=10.1128/MCB.21.13.4292-4301.2001;	
RA Richter B.W.M., Mir S.S., Elden L.J., Lewis J., Raffey S.B.,	
RA Pretetini A., Tian L., Frank S., Youle R.J., Nelson D.L.,	
RA Nocentangelo L.D., Vezzoni P., Fearhead H.O., Duckett C.S.;	
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of	
RT apoptosis protein family.";	
RL Mol. Cell. Biol. 21:4292-4301(2001).	
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By similarity).	
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).	
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).	
CC -1- SIMILARITY: Belongs to the IAP family.	
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.	
CC -----	
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CC modified and this statement is not removed. Usage by and for commercial	
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-----
DR EMBL, AY030053, AAK49777.1; -.
DR HSSP, P98170, I673.
DR InterPro, IPR001370, BIR.
DR InterPro, IPR001841, Znf_ring.
DR Pfam, PF00653, BIR; 1.
DR SMART, SM00228, BIR; 1.
DR SMART, SM00184, RING; 1.
DR PROSITE, PS01282, BIR_REPEAT_1, FALSE_NEG.
DR PROSITE, PS50143, BIR_REPEAT_2, 1.
DR PROSITE, PS00518, ZF_RING_1, FALSE_NEG.
DR PROSITE, PS50089, ZF_RING_2, 1.
DR Apoptosis, zinc-finger.
KM REPEAT 70 BIR.
FT ZN_FING 189 224 RING-type.
SQ SEQUENCE 236 AA; 27120 MW; 63A70E39E8442E4C CRC64;

Query Match 84.2%; Score 325; DB 1; Length 236;
Best Local Similarity 78.8%; Pred. No. 1.8e-30;
Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEALVIFGWTWTSVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDQAKCY 60
DB 4 YEALVIFGWTWTSVYNKEQLARAGFYALGEGDKIKCFHCGGGLANWPKEDPMWGAKMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 12
Q96RW6 ID Q96RW6 PRELIMINARY; PRT; 106 AA.
AC Q96RW6;
DT 01-DEC-2001 (TREMBLrel, 19, Created)
DT 01-DEC-2001 (TREMBLrel, 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel, 24, Last annotation update)
DE IAP-like protein 3.
DE Name=ILP3;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RN [1]
RS SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL, AF164681, AAK81891.1; -.
DR HSSP, P98170, I63F.
DR GO, GO:0005622, C:intracellular; IEA.
DR GO, GO:0006916, P:anti-apoptosis; IEA.
DR InterPro, IPR001370; Prot_inh_132_IAP.
DR Pfam, PF00653, BIR; 1.
DR SMART, SM00238, BIR; 1.
DR PROSITE, PS50143, BIR_REPEAT_2, 1.
SQ SEQUENCE 106 AA; 12360 MW; 6BBAD3AE880A891 CRC64;

Query Match 79.3%; Score 306; DB 2; Length 106;
Best Local Similarity 91.1%; Pred. No. 1.5e-28;
Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 WTSVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDQAKCYPGCKYL 66
DB 2 WTSVYNKEQLSRAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDQKHMPGCKYL 57

RESULT 13
Q8UVF8 ID Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8;
DT 01-MAR-2002 (TREMBLrel, 20, Created)
DT 01-MAR-2002 (TREMBLrel, 20, Last sequence update)

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Query Match	84.2%	Score 325,	DB 1,	Length 236,
Best Local Similarity	78.8%	Pred. No. 1.8e-30,		
Matches 52; Conservative	9;	Mismatches	5;	Indels 0; Gaps 0;

Oy	1	YEAIRVTFPGWITSVNKEOLARAGFYALGEGDKVKCFHCGGLTTPWKPSBEDPMDHAKCY	60
		: : : : : : : : : : : : : : : : :	
Dd	4	YEAMLIITFGTMYSVNKEOLARAGFYAIGEDKRIQCFHCGLGANWKPREDPEMOHAKMY	63
Oy			
	61	PGECKYL	66
Dd		64 PGCKYL	69

QY	61	PGCKYL	66
Db	64	PGCKYL	69

Db 64 PGCKYL 69

[illegible]

Query Match	79.3%	Score 306;	DB 2;	Length 106;
Best Local Similarity	91.1%	Pred. No. 1.5e-26;		
Matches 51; Conservative	3;	Mismatches	2;	Indels 0; Gaps 0;

```

Oy 11 WISYVKEQLBAGFYALGEGDKKCFHCGGGLTDMKPS EDDMDHACVPGCKTL 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 WISYVKEQLSRAGFYALGEGDKKCFHCGGGLTDMKPS EDDMEQHDKWHPGCKTL 57

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Db 2 WIYSVKNQLSRAGFYALGEGDKVACFHCGGGLTDWKPSEDPMEQHDKNHPGCKYL 57

RESULT 13	
Q8UVF8	
ID Q8UVF8	PRELIMINARY;
AC Q8UVF8;	PRT; 493 AA.
DT 01-MAR-2002 (Tremblere1.20, Created)	
DT 01-MAR-2002 (Tremblere1.20, Last Sequence update)	

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DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Inhibitor of apoptosis protein 3.
GN Name=IAP3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF451854; AL47170.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00997; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56C86119BC CRC64;
SO

Query Match 72.3%; Score 279; DB 2; Length 493;
Best Local Similarity 71.2%; Pred. No. 1.2e-24;
Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISVKNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 264 YERRIQTFILAMTIPVKNKEHLAEGFYSTGNDHYVCHCGGLQEMKENEDPMDOHAKMP 323

QY 61 PGCKYL 66
DB 324 PGCKFL 329

RESULT 14
Q8MWY4 PRELIMINARY; PRT; 109 AA.
AC Q8MWY4;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN Name=XIAP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AL466179.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:000622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213D56D CRC64;
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Query Match 66.8%; Score 258; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 8e-23;
Matches 44; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISVKNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 48
DB 57 YEARIYFTGWISVKNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMP 104

RESULT 15
Q6DBV7 PRELIMINARY; PRT; 322 AA.
AC Q6DBV7;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 26, last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zedrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushlt T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078344; AAH78344.1; -.
DR GO; GO:000622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 322 AA; 36412 MW; F9562546FA200CDF CRC64;

Query Match 54.9%; Score 212; DB 2; Length 322;
Best Local Similarity 51.5%; Pred. No. 7.3e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISVKNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 229 FEGRIDSFGRQHPIDPRLIARAGFYSTGNDHYVCHCGGLQEMKENEDPMDOHAKMP 288

QY 61 PGCKYL 66
DB 289 PGCKFL 294
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RESULT 16
08UHM2 PRELIMINARY; PRT; 405 AA.
ID 08UHM2
AC 08UHM2
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Xlap.
GN Name=birc4;
OS Brachydonto rerio (zebrafish) (Danio rerio).
OC Euarystota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Itohara N., Nunez G.;
RT "Gene with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Itohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF439767; ALJ2047.1; -.
DR HSP; P98170; I130.
DR ZFIN; ZDB-GENE-030825-7; birc4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006516; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366342D83BECAB CRC64;

Query Match 54.9%; Score 212; DB 2; Length 405;
Best Local Similarity 51.5%; Pred. No. 9.2e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKY 60
DB 229 FEGRLDSFKGRQHIDPERLARAGFYSTGEGDVMCFRCGGGVKAMPDDEPMEHARHY 288
QY 61 PGCKYL 66
DB 289 PGCSFL 294

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RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Kleeschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helen F.,
RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toohilyukl S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Straubeberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BC055246; AAH55246.1; -.
DR HSP; P98170; I130.
DR ZFIN; ZDB-GENE-030825-7; birc4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006516; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
PT NON TER 1
SQ SEQUENCE 415 AA; 46788 MW; D9B82E448ADDC92 CRC64;

Query Match 54.9%; Score 212; DB 2; Length 415;
Best Local Similarity 51.5%; Pred. No. 9.4e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKY 60
DB 240 FEGRLDSFKGRQHIDPERLARAGFYSTGEGDVMCFRCGGGVKAMPDDEPMEHARHY 289
QY 61 PGCKYL 66
DB 300 PGCSFL 305

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RESULT 18
06UTV9 PRELIMINARY; PRT; 280 AA.
ID 06UTV9
AC 06UTV9
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Choriostoneura fumiferana defective nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OC NCBI_Taxid=74660;
RP SEQUENCE FROM N.A.

```

RN [1]
 RX MEDLINE=20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138;
 RA Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.;
 RT "Characterization of an overexpressed spindle protein during a
 RT baculovirus infection.";
 RL virology 268:56-67(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: AY327402; A091688.1;
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001370; Prot inh_132_IAP.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00653; BIR; 2.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 2.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 280 AA; 32179 MW; CA804614BFDPIAL CRC64;
 Query Match 52.8%; Score 204; DB 2; Length 280;
 Best Local Similarity 51.5%; Pred. No. 5.7e-16;
 Matches 34; Conservative 14; Mismatches 16; Indels 2; Gaps 1;
 QY 3 ARIVFGTWYSVVK--EQIARAGFYALGSGDKVCFHCGSGULTWKPSPMDQAKCY 60
 DB 115 ARKTFVDMVSLKQKQKQGLAELAGFYTGKGRKCHCQGLKDWESTDEPNEHARMF 174
 QY 61 PGCKYL 66
 DB 175 DRCTYV 180
 RESULT 19
 BIR3_HUMAN STANDARD; PRT; 604 AA.
 ID BIR3_HUMAN
 AC Q13489; Q16628; Q9HC27; Q9UP46;
 DT 01-NOV-1997 (Ref. 35, Created)
 DT 01-NOV-1997 (Ref. 35, Last sequence update)
 DT 05-JUL-2004 (Ref. 44, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis
 DE protein 1) (IAP homolog C) (C-IAP2) (TNFR2-TRAF signaling complex
 GN Name-BIRC3; Synonyms-AP12, IAP1, MIRH;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9618127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
 RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related
 RT to baculoviral inhibitor of apoptosis proteins.";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9619249; PubMed=8557191; DOI=10.1038/379349a0;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Bald S., Chertou-Horvat G.,
 RA Farahani R., McLean M., Ikeda Y., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";

RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96209883; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
 RX Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
 RA "Cloning and expression of apoptosis inhibitory protein homologs that
 RT function to inhibit apoptosis and/or bind tumor necrosis factor
 RT receptor-associated factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99252096; PubMed=10233894;
 RA Horrevoets A.J., Fontijn R.D., Van Zonneveld A.J., de Vries C.J.,
 RA ten Cate J.W., Pannekoek H.;
 RT "Vascular endothelial genes that are responsive to tumor necrosis
 RT factor-alpha in vitro are expressed in atherosclerotic lesions,
 RT including inhibitor of apoptosis protein-1, stannin, and two novel
 RT genes.";
 RL Blood 93:3418-3431(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA TISSUE=lymph;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carminci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wallat S.J.,
 RA Hosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Vailion D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feiley J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 362-441 FROM N.A.
 RX MEDLINE=20519161; PubMed=11066071;
 RX DOI=10.1002/1098-2264(2000)9999:9999<:AID-GC1036>3.0.CO;2-I;
 RA Baens M., Steyts A., Dierlamm J., De Wolf-Peters C., Marynen P.;
 RT "Structure of the MTR gene and molecular characterization of the
 RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
 RT B-cell lymphomas of MALT type.";
 RL Genes Chromosomes Cancer 29:281-291(2000).
 CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
 CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
 CC form an heteromeric complex, which is then recruited to the tumor
 CC necrosis factor receptor 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: Highly expressed in fetal lung, and kidney. In
 CC the adult, expression is mainly seen in lymphoid tissues,
 CC including spleen, thymus and peripheral blood lymphocytes.
 CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
 CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
 CC tissue). This translocation is found in approximately 50% of
 CC cytogenetically abnormal low-grade MALT lymphoma and involves
 CC MALT1 and BIRC3.
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;

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CC      WWW="http://www.infobiogen.fr/services/chromcancer/genes/BIRC3ID239.html".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC      or send an email to license@1sb-sib.ch).
CC      -----
DR      EMBL; LA9432; AAC41943.1; -
DR      EMBL; U45878; AAC50371.1; -
DR      EMBL; U37546; AAC50507.1; -
DR      EMBL; AF070674; AAC83232.1; -
DR      EMBL; BC037420; AAC37420.1; -
DR      EMBL; AF178945; AAC09369.1; -
DR      PIR; S68449; S68449.
DR      HSSP; Q13490; IOBH.
DR      Genew; HGNC:591; BIRC3.
DR      MIM; 601721; -
DR      GO; GO:0005515; F:protein binding; NAS.
DR      GO; GO:0006916; P:anti-apoptosis; TAS.
DR      GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR      InterPro; IPR001370; BIR.
DR      InterPro; IPR001315; CARD.
DR      InterPro; IPR01029; DEATH_1ike.
DR      InterPro; IPR001841; Znf_ring.
DR      Pfam; PF00653; BIR; 3.
DR      Pfam; PF00619; CARD; 1.
DR      Pfam; PF00097; zf-C3HC4; 1.
DR      SMART; SM00238; BIR; 3.
DR      SMART; SM00114; CARD; 1.
DR      SMART; SM00184; RING; 1.
DR      PROSITE; PS01282; BIR_REPEAT_1; 3.
DR      PROSITE; PS50143; BIR_REPEAT_2; 3.
DR      PROSITE; PS50209; CARD; 1.
DR      PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE; PS50089; ZF_RING_2; 1.
DR      Apoptosis; Chromosomal translocation; Repeat; Zinc-finger.
DR      REPEAT 29 96 BIR 1.
DR      REPEAT 169 235 BIR 2.
DR      REPEAT 255 322 BIR 3.
DR      DOMAIN 439 529 CARD.
DR      ZN_FING 557 592 CARD.
DR      STR 442 443 BIRC3-MATRL.
DR      FT CONFLICT 18 18 N -> Y (in Ref. 4).
DR      FT CONFLICT 119 119 N -> H (in Ref. 2).
DR      FT CONFLICT 153 153 D -> E (in Ref. 2).
DR      FT CONFLICT 163 163 H -> P (in Ref. 2).
DR      FT CONFLICT 165 165 A -> P (in Ref. 2).
DR      FT CONFLICT 191 191 K -> R (in Ref. 2).
DR      FT CONFLICT 364 364 F -> L (in Ref. 2).
DR      FT CONFLICT 552 552 Q -> P (in Ref. 2).
DR      FT CONFLICT 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;
SQ      SEQUENCE
Query Match 51.3%; Score 198; DB 1; Length 604;
Best Local Similarity 55.9%; Pred. No. 6,4e-15;
Matches 39; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
QY 1 YEARIYVGTWIVS--VVKQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDQHAQ 58
Db 255 HAARFKTFEWMPSVLVNPQLASAGFYVGNSDVACFCDDGLRCMESGDDPWQVQHAQ 314
QY 59 CYPGCKYL 66
Db 315 WPRCEYL 322
RESULT 20
Q6E7G7 PRELIMINARY; PRT; 287 AA.
AC Q6E7G7;

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DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE IAP-3.
OS Anticarsa gemmatilis nuclear polyhedrosis virus (AgMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=31507;
RN [1]
RP SEQUENCE FROM N.A.
RA Carpes M.P., Castro M.E., Soares E.F., Villela A.G., Plinedo F.J.,
RA Ribeiro B.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525121; AAS92269.1; -
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006316; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 287 AA; 32620 MW; 20F3A7F0C11C4C2B CRC64;
Query Match 50.8%; Score 196; DB 2; Length 287;
Best Local Similarity 50.0%; Pred. No. 5.2e-15;
Matches 33; Conservative 14; Mismatches 17; Indels 2; Gaps 1;
QY 3 ARIVTGTWIVSYNK--EQIARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDQHAQ 60
Db 127 ARKTFEDNPLSLKQRPQLAEAGFYVTKGDKVKCFCDGGLKQVAMNDEPHEHARWF 166
QY 61 PGCKYL 66
Db 187 DRCSFV 192
RESULT 21
PIAP_PIG STANDARD; PRT; 358 AA.
AC 062630;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative inhibitor of apoptosis.
GN Name=PIAP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adip;
RX MEDLINE=9816262; PubMed=9501011; DOI=10.1006/bbrc.1998.8185;
RA Stenlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis protein
RT (IAP) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 2 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC EMBL: U79142; AAC39171.1; -.
DR PIR: JCS964; JCS964.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR01841; Znf_ring.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Repeat; Zinc-finger.
DR REPEAT 4 70 BIR 1.
DR REPEAT 90 157 BIR 2.
DR DOMAIN 193 283 CARD.
DR ZN_RING 311 346 RING-type.
SO SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 50.8%; Score 196; DB 1; Length 358;
Best Local Similarity 54.4%; Pred. No. 6.6e-15;
Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFGTWIS--VNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQHA 58
Db 90 YAAKFKTFPCWPPSSIPVHPQLASAGFYVMGHSDPVKCFCCDGLRCWESGDDPWVHAHAK 149
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poul. Sci. 80:284-288(2001).
DR EMBL: AF221083; AAF35320.1; -.
DR HSSP: Q13490; 10BH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
FT NON TER 1 1
FT NON TER 195 195
SO SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

RESULT 22
ID O91A70 PRELIMINARY; PRT; 195 AA.
AC O91A70;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Leghorn; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poul. Sci. 80:284-288(2001).
DR EMBL: AF221082; AAF35319.1; -.
DR HSSP: Q13490; 10BH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
FT NON TER 1 1
FT NON TER 195 195
SO SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

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Query Match 49.7%; Score 192; DB 2; Length 195;
Best Local Similarity 52.9%; Pred. No. 1.1e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFGTW--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQHA 58
Db 116 HEARKVTFINWPRIPVQPEQLADAGFYVMGRNDVKCFCCDGLRCWESGDDPWVHAHAK 175
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poul. Sci. 80:284-288(2001).
DR EMBL: AF221083; AAF35320.1; -.
DR HSSP: Q13490; 10BH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
FT NON TER 1 1
FT NON TER 197 197
SO SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 49.7%; Score 192; DB 2; Length 197;
Best Local Similarity 52.9%; Pred. No. 1.1e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFGTW--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQHA 58
Db 117 HEARKVTFINWPRIPVQPEQLADAGFYVMGRNDVKCFCCDGLRCWESGDDPWVHAHAK 176
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poul. Sci. 80:284-288(2001).
DR EMBL: AF221083; AAF35320.1; -.
DR HSSP: Q13490; 10BH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
FT NON TER 1 1
FT NON TER 197 197
SO SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

RESULT 24
ID O9ESB9 PRELIMINARY; PRT; 602 AA.
AC O9ESB9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

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[1]
RN SEQUENCE FROM N.A.
RP PubMed=11860601;
RA Hocking M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
of Apoptosis protein 1, 2, and 3 genes";
RL BMC Genomics 3:5-5(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF183430; AAC22970.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004942; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR01315; CARD.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM0037; ZF_C3HC4; 1.
DR SMART; SM0038; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; zinc; Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EBA62DE5A CRC64;

Query Match 49.7%; Score 192; DB 2; Length 602;
Best Local Similarity 51.5%; Pred. No. 3.3e-14;
Matches 35; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIYVFGTWYS--VNKQLARAGFYALGEGDKYKCFGCGGLTDMKPSDEPMDQAK 58
DB 255 HAARVRFSTWPSALVHPOLASAGTYTGSHSDVACFCDCGLRCWESGDDPWTEHAK 314
QY 59 CYPGCKXTL 66
DB 315 WPPRCCEYL 322

RESULT 25
BIR_CHICK
ID_BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660; 057319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
protein).
GN Name=ITA; Synonyms=IAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9710112; PubMed=8945639;
RA Digby M.R., Kilmpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
lymphocytes.";
RL DNA Cell Biol. 15:981-986(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Embryonic fibroblast;

RX MEDLINE=98038801; PubMed=9372964;
RA You M., Xu P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
mediator of the antiapoptotic activity of the v-Rel oncoprotein";
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: Apoptotic suppressor.
CC -1- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic according
to Ref.2.
CC -1- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in
both cortical and medullary cells of the thymus. Expressed at
relatively high levels also in spleen, bursa, intestine and lung
and at very low levels in testis, brain and skeletal muscle.
CC -1- INDUCTION: High levels are induced within 4-8 hours of T-cell
activation in spleen and thymus.
CC -1- DOMAIN: The ring finger is important for its antiapoptotic effect.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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DR EMBL; U27466; AAB48118.1; -.
DR EMBL; AF008592; AAB88044.1; -.
DR HSSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01282; BIR_REPEAT_2; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS5018; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Nuclear protein; Repeat; Zinc-finger.
KM REPEAT 30
FT REPEAT 176 242 BIR 1.
FT REPEAT 262 329 BIR 2.
FT REPEAT 446 536 BIR 3.
FT ZN_FING 564 599 CARD.
FT CONFLICT 27 27 RING-type.
FT CONFLICT 150 150 R -> L (in Ref. 2).
FT CONFLICT 169 169 R -> Q (in Ref. 2).
FT CONFLICT 183 183 O -> H (in Ref. 2).
FT CONFLICT 190 192 S -> F (in Ref. 2).
FT CONFLICT 192 192 CW -> FLS (in Ref. 2).
FT CONFLICT 196 196 V -> L (in Ref. 2).
FT CONFLICT 202 203 DD -> YY (in Ref. 2).
FT CONFLICT 213 214 VN -> FT (in Ref. 2).
FT CONFLICT 217 218 VK -> GQ (in Ref. 2).
FT CONFLICT 350 355 WNSGCT -> EQLS (in Ref. 2).
FT CONFLICT 359 359 K -> T (in Ref. 2).
FT CONFLICT 426 426 E -> D (in Ref. 2).
FT CONFLICT 492 492 T -> K (in Ref. 2).
FT CONFLICT 497 497 S -> L (in Ref. 2).
FT CONFLICT 524 524 F -> C (in Ref. 2).
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 49.7%; Score 192; DB 1; Length 611;
Best Local Similarity 52.9%; Pred. No. 3.4e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFGTW--IYVNKQLARAGFYALGEGDKYKCFGCGGLTDMKPSDEPMDQAK 58
DB 262 HAARVRFSTWPSALVHPOLASAGTYTGSHSDVACFCDCGLRCWESGDDPWTEHAK 321

QY 59 CYECKYL 66
 Db 322 WPRCEYL 329

RESULT 26

IAP3_NPVOP STANDARD; PRT; 268 AA.
 ID IAP3_NPVOP
 AC PA1437;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Apoptosis inhibitor 3 (IAP-3).
 GN Name=IAP3; Synonyms=IAP;
 OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187094; PubMed=8139034;
 RA Birnbaum M.J., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
 RT encoding a polypeptide with Cys/His sequence motifs.";
 RL J. Virol. 68:2521-2528(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126251; DOI=10.1006/viro.1997.8448;
 RA Ahrens C.H., Ruessell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
 RT polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 RN [3]
 RP INTERACTION WITH HUMAN PDC13.
 RX PubMed=15371430; DOI=10.1074/jbc.M409623200;
 RA Wilkinson J.C., Richter B.W.M., Wilkinson A.S., Burretein E.,
 RA Rumble J.M., Ballin B., Duckett C.S.;
 RT "VIAF, a conserved inhibitor of apoptosis (IAP) interacting factor
 RT that modulates caspase activation.";
 RL J. Biol. Chem. 279:0-0(2004).
 CC -I- FUNCTION: Acts by blocking cellular apoptosis rather than by
 CC preventing viral stimulation of apoptosis.
 CC -I- SUBUNIT: Interacts with human PDC13.
 CC -I- SIMILARITY: Contains 2 BIR repeats.
 CC -I- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC EMBL; L22564; AAB02610.1; -;
 DR EMBL; U75930; AAC5903.1; -;
 DR PIR; A53989; A53989.
 DR HSSP; Q24306; IJD4.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 2.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00238; BIR; 2.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 2.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM Apoptosis; Repeat; zinc-finger.
 FT REPEAT 18 84 BIR 1.
 FT REPEAT 111 178 BIR 2.

FT ZN RING 221 256 RING-type.
 SQ SEQUENCE 268 AA; 30076 MW; DE89175FDEB85A708 CRC64;
 Query Match 49.2%; Score 190; DB 1; Length 268;
 Best Local Similarity 48.5%; Pred. No. 2, 5e-14;
 Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVFGTWISYVNK--EQLARAGFYALGEGDVKCFHCGGLTDWKPSEDPMDQAHKC 60
 Db 113 ARIRTFEAWPRGKQRPBEILAEAGFFYTGQDKTRCFCCDGGILKDWEPDDAPWQOHARWY 172

QY 61 PGCKYL 66
 Db 173 DRCEYV 178

RESULT 27

O6OXJ6 PRELIMINARY; PRT; 269 AA.
 ID O6OXJ6
 AC O6OXJ6;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE OREF53.
 GN Name=OREF53; IAP-1; ORENames=AgVp053;
 OS Agrotis segetum granulosus virus (AgGV) (Agrotis segetum
 OC granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=10464;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Yuhu S., Mei H.;
 RT "Agrotis segetum Granulosis Virus complete genome.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Al X.L., Wang Z.F., Wang B., Zhang W., Li F., Fu J.H., Cui C.S.,
 RA Shi Y.H., He M.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Yuhu S., Mei H.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY522332; AAS82685.1; -;
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001370; Prot_inh_132_IAP.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 2.
 DR SMART; SM00238; BIR; 2.
 DR PROSITE; PS01282; BIR_REPEAT_1; 1.
 DR PROSITE; PS50143; BIR_REPEAT_2; 2.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 269 AA; 31135 MW; C929C533465BEC51 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 269;
 Best Local Similarity 47.8%; Pred. No. 3, 4e-14;
 Matches 32; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVFGTWISV--NKEQLARAGFYALGEGDVKCFHCGGLTDWKPSEDPMDQAHKC 59
 Db 115 ENRLESYKTPWPSIPLRPKELAAAGFYTGHSDDVNVCFCGGLKDWKTDGDDPMDQHARW 174


```
Db          313 WPRCEYL 320

RESULT 30
0804E2      PRELIMINARY;      PRT: 616 AA.
ID 0804E2
AC 0804E2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN Name=IAP-1;
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Praveen K., Leary J.H. III, Evans D.L., Jaseo-Friedmann L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY184377; AAC24632.1; -.
DR HSSP; Q13490; 10BH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0042881; P:regulation of apoptosis; IEA.
DR GO; GO:0001315; CARD.
DR InterPro; IPR001029; DEATH_1like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KM SEQUENCE 616 AA; 69546 MW; D1389D915C6B256 CRC64;
SQ

Query Match          49.0%; Score 189; DB 2; Length 616;
Best Local Similarity 50.7%; Pred. No. 7.7e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTFGTW--IYSVNKEQLARAGFYALGEGDKVKGCGGLITWKPSEDDPWMDHAKC 59
DB 270 EERLLTFVWMPARIPRPDQLAKAGFYVGRNDVVKCFCCDGLRCWESGDDPWVGHAKW 329
QY 60 YPGCKYL 66
DB 330 FPRCEYL 336

RESULT 31
0804E2      PRELIMINARY;      PRT: 628 AA.
ID 0804E2
AC 0804E2;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Iap1.
GN Name=birc3; Synonyms=iap1;
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ems K.M., Valdimarsson G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY247786; AAP04483.1; -.
DR HSSP; P98170; 1130.
DR ZFIN; ZDB-GENE-030825-6; birc3.
```

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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RT Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF442500; AAL33679.1; -.
DR HSSP; Q13490; 10BH.
DR ZFIN; ZDB-GENE-030825-6; birc3.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0042881; P:regulation of apoptosis; IEA.
DR GO; GO:0001315; CARD; 3.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DM Metal-binding; Zinc; Zinc-finger.
KM SEQUENCE 628 AA; 70098 MW; 5B68C6B6A87C8A95 CRC64;
SQ

Query Match          49.0%; Score 189; DB 2; Length 628;
Best Local Similarity 50.7%; Pred. No. 7.9e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTFGTW--IYSVNKEQLARAGFYALGEGDKVKGCGGLITWKPSEDDPWMDHAKC 59
DB 280 EERLLTFVWMPARIPRPDQLAKAGFYVGRNDVVKCFCCDGLRCWESGDDPWVGHAKW 339
QY 60 YPGCKYL 66
DB 340 FPRCEYL 346

RESULT 32
0770K2      PRELIMINARY;      PRT: 647 AA.
ID 0770K2
AC 0770K2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=birc3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ems K.M., Valdimarsson G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY247786; AAP04483.1; -.
DR HSSP; P98170; 1130.
DR ZFIN; ZDB-GENE-030825-6; birc3.
```

DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; F:anti-apoptosis; IEA.
DR GO: GO:0016567; F:protein ubiquitination; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH like.
DR InterPro: IPR001370; ProtInh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 647 AA; 72183 MW; 868DBAFB92718FA9 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 647;
Best Local Similarity 50.7%; Pred. No. 8.1e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSDDPMDQAKC 59
DB EERLITFTVNMPSRIPIRPDQLAKAGFYVGRNDVVCFCDDGGLRCWESGDDPWEHAKW 358
QY 60 YPGCKYL 66
DB 359 FPRCEYL 365

RESULT 33

Q6ZM93 PRELIMINARY; PRT; 654 AA.
AC Q6ZM93
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE St: bz1p1.6.2 (Baculoviral IAP repeat-containing 3).
GN Nemeb1rc3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AL627325; CA647763.1; -
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; F:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH like.
DR InterPro: IPR001370; ProtInh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 654 AA; 72995 MW; A12425DE41A0359 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 654;
Best Local Similarity 50.7%; Pred. No. 8.2e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSDDPMDQAKC 59
DB EERLITFTVNMPSRIPIRPDQLAKAGFYVGRNDVVCFCDDGGLRCWESGDDPWEHAKW 365
QY 60 YPGCKYL 66
DB 366 FPRCEYL 372

RESULT 34

Q8IS31 PRELIMINARY; PRT; 346 AA.
AC Q8IS31
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxId=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY155274; AAN46650.1; -
DR HSP: Q24306; 1040.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; F:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; ProtInh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR SEQUENCE 346 AA; 36849 MW; 5450EB75F56A8486 CRC64;

Query Match 47.9%; Score 185; DB 2; Length 346;
Best Local Similarity 47.0%; Pred. No. 1.3e-13;
Matches 31; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSDDPMDQAKC 60
DB ARLATFDWDRCKRQKPELAEAGFYVGTGDKTKCFYCDGGLKDWESDDPWEHARWF 243
QY 61 PGCKYL 66
DB 244 DRCAVY 249

RESULT 35

Q968T8 PRELIMINARY; PRT; 346 AA.
AC Q968T8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

```
DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DE Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotia;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
NCBI_TaxId=7091;
RN
  [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1240184; PubMed=1134196; DOI=10.1016/S0167-4889(00)00105-1;
RA Huang Q., Deveraux Q.L., Maeda S., Stenicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) from Bombyx mori.";
RL Blochm. Biophys. Acta 1499:191-198(2001).
DR EMBL; AF281073; AAK57560.1; -.
DR HSSP; Q24306; 104Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Proc_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00184; RING; 1.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CF6C6468894C69 CRC64;

Query Match          47.9%; Score 185; DB 2; Length 346;
Best Local Similarity 47.0%; Pred. No. 1.3e-13;
Matches 31; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVFGTWIYVSNK--EQARAGFYALGEGDKVCKFHCGGLTDMKPSDPMDOHAKY 60
DB 184 ARLATFMDWRMRQRKPEBELAEGFFVTGGQDKKCYCGGLKDMESDVPMEQHARWF 243
QY 61 PGCKYL 66
DB 244 DRCAVY 249

RESULT 36
Q9ESB8 PRELIMINARY; PRT; 589 AA.
AC Q9ESB8;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;
RN
  [1]
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes.";
RL BMC Genomics 3:5-5(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF183431; AAG2871.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
```

```
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR01029; DEATH_1like.
DR InterPro; IPR001370; Proc_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match          47.9%; Score 185; DB 2; Length 589;
Best Local Similarity 51.5%; Pred. No. 2.2e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYFGTWIYS--VNKEQLARAGFYALGEGDKVCKFHCGGLTDMKPSDPMDOHAK 58
DB 241 HSARMSFTFLWPSVVLVQPEQLASAGFYVDHNDVCKFCFCDCGLRCWBERGDDPMTEHAK 300
QY 59 CYPCKYL 66
DB 301 WPRCEPL 308

RESULT 37
Q9QZC6 PRELIMINARY; PRT; 589 AA.
ID Q9QZC6;
AC Q9QZC6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;
RN
  [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22020585; PubMed=12023884; DOI=10.1042/BJ20011431;
RA Dong Z., Nishiyama Y., Yi X., Venkatchalam M.A., Denton M., Gu S.,
RA Li S., Qiang M.;
RT "Gene promoter of apoptosis inhibitory protein IAP2: identification of
RT enhancer elements and activation by severe hypoxia.";
RL Biochem. J. 364:413-421(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF190020; AAF04585.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR01029; DEATH_1like.
DR InterPro; IPR001370; Proc_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
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CC or send an email to license@isb-sib.ch).

DR	EMBL	U49433	AAC42078.1	-	
DR	EMBL	U08909	AAC53532.1	-	
DR	HSSP	Q13490	IQBH		
DR	MGD	MGI1197009	Bioc3in		
DR	GO	GO:0005515	P:protein binding; IPI		
DR	InterPro	IPR0013370	BIR		
DR	InterPro	IPR001335	CARD		
DR	InterPro	IPR011029	DEATH_like		
DR	InterPro	IPR001841	Znf_ring		
DR	Pfam	PF00653	BIR: 3		
DR	Pfam	PF00619	CARD: 1		
DR	Pfam	PF00097	zf-C3HC4	1	
DR	SMART	SM00238	BIR: 3		
DR	SMART	SM00114	CARD: 1		
DR	SMART	SM00184	RING: 1		
DR	PROSITE	PS01282	BIR_REPEAT_1	3	
DR	PROSITE	PS50143	BIR_REPEAT_2	3	
DR	PROSITE	PS50209	CARD: 1		
DR	PROSITE	PS00518	zf_RING_1	FALSE_NEG	
DR	PROSITE	PS50089	zf_RING_2	1	
DR	APOLLO18	Direct protein sequencing; Repeat; Zinc-finger			
FT	REPEAT	46	113	BIR 1.	
FT	REPEAT	177	243	BIR 2.	
FT	REPEAT	262	329	BIR 3.	
FT	ZN_DOMAIN	447	537	CARD.	
FT	ZN_RING	565	600	RING-type.	
FT	CONFLICT	380	380	E -> K (in Ref. 2).	
SQ	SEQUENCE	612 AA;	65676 MW;	E08969D93C6C610D	CRC64;

Query Match	47.7%	Score 184;	DB 1;	Length 612;
Best Local Similarity	51.5%	Pred. No. 3e-13;		
Matches 35; Conservative	9;	Mismatches 22;	Indels 2;	Gaps 1;

QY	1	YEARLITFGWITS--VNKEQLARAGFYALGEGDKYKCFHCGGGLITDKRPEEDPMWQIAK	58
	:	:::::	:::::
	:	:	:
Db	262	HSARLRTFLYMPSPVPEQPEQLASAGFYVVDNDVDKCECCDGGRLCMERPEDDPMIEIAK	322
QY	59	CYPGCKYL	66
	:	:::::	:::::
Db	322	WPERCEFL	329

RESULT 40	081Z20	PRELIMINARY;	PRT;	534 AA.
ID	081Z20;			
AC	081Z20;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)			
DE	Pdb-interacting protein Rbap-36.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph node;			
RA	Pen Z.S., Mo S.Z.;			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF207559; AAN73272.1; -			
DR	HSSP; Q13490; IOBH.			
DR	GO; GO:0005622; C:intracellular; IEA.			
DR	GO; GO:0005515; F:protein binding; IEA.			
DR	GO; GO:0006916; P:anti-apoptosis; IEA.			
DR	GO; GO:0042981; P:regulation of apoptosis; IEA.			
DR	InterPro; IPR001315; CANTD.			

DR InterPro: IPR011029; DEATH like.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam; PF00663; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01043; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
SQ SEQUENCE 534 AA; 60366 MW; 0403170475BE0872 CRC64

Query Match	47.4%;	Score 183;	DB 2;	Length 534;
Best Local Similarity	51.5%;	Pred. No. 3.5e-13;		
Matches 35; Conservative	9;	Mismatches 22;	Indels 2;	Gaps 1;

[illegible]

Search completed: June 15, 2005, 17:39:35
Job time : 115.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:18:26 ; Search time 115 Seconds
(without alignments)

221.967 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389

Sequence: 1 YEARIPTFTGWTIVSVNKEQL.....KPSEDPWEQHAQKYPGCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	389	100.0	66	7 ADB61810 Human inh
2	389	100.0	110	8 ADP90805 ADP90805 Human XIA
3	389	100.0	236	5 ABG32418 X-linked
4	389	100.0	278	5 AAO20511 Protein o
5	389	100.0	497	2 AA019581 Human apo
6	389	100.0	497	2 AA069294 Human XIA
7	389	100.0	497	3 AAY59451 Human XIA
8	389	100.0	497	3 AAY99985 Human X-1
9	389	100.0	497	5 ABG65663 Human inh
10	389	100.0	497	5 ADB80961 RING-SH C
11	389	100.0	497	7 AD139804 Human inh
12	389	100.0	497	8 ADH74639 Human XIA
13	389	100.0	497	8 ADL70166 Human X c
14	389	100.0	497	8 ADP23982 PRO polyp
15	389	100.0	497	8 ADB61827 Rat inhib
16	368	94.6	496	2 AA019745 Mouse inh
17	366	94.1	496	2 AA019584 Mouse apo
18	366	94.1	496	2 AA069297 Murine XI
19	366	94.1	496	5 ABG65666 Mouse inh
20	352	90.5	66	7 ADB61828 Mouse inh
21	352	90.5	496	6 ABP72157 Mouse inh
22	347	89.2	66	7 ADB61820 Human inh
23	347	89.2	236	5 AAY81440 Human TIA
24	347	89.2	236	5 AA00365 Human IAP
25	347	89.2	236	5 AAU75066 Human tes

26	347	89.2	236	5 ABG32417 Inhibitor
27	347	89.2	464	5 AAU75747 Human inh
28	342.5	88.0	87	8 AD044576 X-IAP BIR
29	341	87.7	236	4 AA00366 Chimpanze
30	338	86.9	66	7 ADB61831 Gorilla i
31	338	86.9	236	4 AA00367 Gorilla i
32	332	82.8	57	7 ADB61832 Unidentif
33	295	75.8	53	7 AD139821 Human NAI
34	287	73.8	66	7 ADB61829 Chicken i
35	273	70.2	151	5 ADK34975 Novel hum
36	255	65.6	52	7 ADB61830 Bovine in
37	216	55.5	68	7 ADB61833 Zebra fib
38	211	54.2	68	7 ADB61813 Human inh
39	211	54.2	442	8 AD026592 Human API
40	211	54.2	557	6 ABP72159 Inhibitor
41	211	54.2	604	2 AA019582 Human apo
42	211	54.2	604	2 AA019747 Human inh
43	211	54.2	604	2 AA019546 Human c-i
44	211	54.2	604	2 AA069295 Human HIA
45	211	54.2	604	2 AAY52703 Human cel

ALIGNMENTS

RESULT 1	ADB61810
ID	ADB61810 standard; protein; 66 AA.
XX	AC ADB61810;
XX	DT 04-DEC-2003 (first entry)
XX	DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX	XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
XX	XX apoptosis pathway; embryonic development; viral pathogenesis; cancer;
XX	XX autoimmune disorder; neurodegenerative disease; apoptotic response;
XX	XX systemic lupus erythematosus; multiple sclerosis; viral infection;
XX	XX herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
XX	XX HRAPI, CIAP2; HIRAP; CIAP1; RING zinc finger; caspase-7;
XX	XX caspase-9; cytotoxic; neoplasm; leukaemia; colon carcinoma;
XX	XX cervical cancer; uterine cancer; testicular cancer;
XX	XX small cell lung carcinoma; uterine cancer; renal cell carcinoma;
XX	XX Wilms' tumor; human; BIR 3 domain.
OS	Homo sapiens.
XX	XX WO2003040172-A2.
XX	XX 15-MAY-2003.
XX	XX 12-NOV-2002; 2002WO-CA001738.
XX	XX 09-NOV-2001; 2001US-0332300P.
XX	XX 08-APR-2002; 2002US-0370934P.
XX	XX (AEGF-) AEGERA THERAPEUTICS INC.
PA	PA Boudreaux A, Korneluk RG, La Casse E, Létton P,
XX	XX WPI; 2003-513532/48.
DR	DR Polypeptide capable of forming a complex with a polypeptide comprising a
PT	PT baculovirus inhibitor of apoptosis repeat domain useful for treating a
PT	PT cancer and other neoplasms.
XX	XX Disclosure; Fig 1A; 53p; English.
PS	PS This invention relates to a substantially pure polypeptide having a
CC	CC length of less than 100 amino acids and capable of forming a complex with
CC	CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC	CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (cIAP2) and HAPI2 (cIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

XX Sequence 66 AA;

Query Match 100.0%; Score 389; DB 7; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.7e-39; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
 Db 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60

QY 61 PGCKYTL 66
 Db 61 PGCKYTL 66

RESULT 2
 ADP90805
 ID ADP90805 standard; peptide; 110 AA.

XX ADP90805;

DT 09-SEP-2004 (first entry)

DE Human XIAP protein BIR-3 domain.

XX protein labelling; peptide labelling;

KM irreversible affinity tagging residue;

KM pharmaceutical agent; human; XIAP; BIR-3.

XX Homo sapiens.

PN WO2004051270-A2.

PD 17-JUN-2004.

PF 04-DEC-2003; 2003WO-EP013715.

PR 05-DEC-2002; 2002GB-00028429.

PA (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS PHARMA GMBH.

PI Auer M, Meisner N, Selfert J;

DR WPI; 2004-480677/45.

PT Providing labeled target protein or target peptide by contacting chemical
 compound with affinity support, removing impurities in reaction mixture
 PT surrounding affinity support, cleaving or eluting chemical molecule from
 PT affinity support.

PS Example 6; Page 46; 81pp; English.

XX The invention comprises a method for providing a labelled target
 CC protein/peptide. The method involves contacting a chemical compound with
 CC affinity support, removing impurities in the reaction mixture surrounding
 CC the affinity support to which the chemical molecule is bound, and
 CC cleaving or eluting the molecule from the affinity support to obtain
 CC irreversible or reversible affinity tagging residue, labelled target
 CC protein or labelled peptide. The method of the invention is useful for
 CC labelling a target protein/peptide or high throughput screening assay.
 CC The method of the invention is useful for identifying agents that
 CC modulate the activity or characteristics of a target protein/peptide -
 CC such agents are useful as pharmaceuticals. The present amino acid
 CC sequence represents the BIR-3 domain from the human XIAP protein which
 CC was used in an example of the invention.

XX Sequence 110 AA;

Query Match 100.0%; Score 389; DB 8; Length 110;
 Best Local Similarity 100.0%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
 Db 17 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 76

QY 61 PGCKYTL 66
 Db 77 PGCKYTL 82

RESULT 3
 ABG32418
 ID ABG32418 standard; protein; 236 AA.

XX ABG32418;

DT 15-NOV-2002 (first entry)

DE X-linked inhibitor of apoptosis protein, XIAP.

XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;

KM fertility; testicular cancer; male infertility; male birth control;

XX X-linked inhibitor of apoptosis protein; XIAP.

OS Mammalia.

FT Key Location/Qualifiers

FT Misc-difference 1 /note="Encoded by mm; start codon is illegible in

FT specification"

PN US2002086409-A1.

PD 04-JUL-2002.

PF 18-DEC-2001; 2001US-00024433.

PR 29-JAN-1998; 98US-0073001P.

XX 29-JAN-1999; 99US-00239867.

PA (KORU/) KORNEJUK R G.

XX (LAGA/) LAGACE M.

PI Kornejuk RG, Lagace M;

DR WPI; 2002-642245/69.

XX N-PSDB; ABS52803.

PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins

PT that is expressed in testes useful for modulating apoptosis in cells,

PT particular cells involved in male fertility.

PS Example 3; Fig 4B; 24pp; English.

XX A substantially pure TIAP polypeptide (1), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (1) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (1) is useful for increasing apoptosis in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (1) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the amino
 CC acid sequence of X-linked inhibitor of apoptosis protein, XIAP

XX Sequence 236 AA;

Query Match 100.0%; Score 389; DB 5; Length 236;

Best Local Similarity 100.0%; Pred. No. 7.5e-39; Mismatches 0; Indels 0; Gaps 0;

Matches 66; Conservative 0; Indels 0; Gaps 0;
 QY 1 YEARIFFFGTWIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDWKPSPDPMQHAQMY 60
 DB 4 YEARIFFFGTWIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDWKPSPDPMQHAQMY 63

QY 61 PGCKYL 66
 DB 64 PGCKYL 69

RESULT 4

AAO20511 ID AAO20511 standard; protein; 278 AA.

XX AAO20511;

DT 27-JUN-2002 (first entry)

XX Protein of APP related human homologue hCP35211.

XX Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KM amyloid precursor protein; tissue-specific expression control; human APP;
 KM APP pathway modulator; gene therapy.

XX Homo sapiens.

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.

XX 14-JUN-2001; 2001US-0298309P.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MMH, Zuesman S;

XX WPI; 2002-315796/35.

XX N-PSDB; AAK99405.

XX New transgenic fly, containing DNA encoding an Abeta portion of human
 PT APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease.

XX Example 4; Page 112; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-

CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This sequence represents the
 CC protein of the APP related human homologue hCP35211

XX Sequence 278 AA;

Query Match 100.0%; Score 389; DB 5; Length 278;

Best Local Similarity 100.0%; Pred. No. 9e-39; Mismatches 0; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIFFFGTWIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDWKPSPDPMQHAQMY 60
 DB 46 YEARIFFFGTWIYSVNKEQLARAGFYALGSDKVKCFHCGGGLTDWKPSPDPMQHAQMY 105

QY 61 PGCKYL 66
 DB 106 PGCKYL 111

RESULT 5

AAW19581 ID AAW19581 standard; protein; 497 AA.

XX AAW19581;

DT 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor XIAP.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
 KM AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
 KM myocardial infarction; stroke; reperfusion injury;
 KM toxin-induced liver disease; gene therapy; diagnosis.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.
 PS Claim 27; Page 68-70; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a zinc
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 CC
 XX Sequence 497 AA:
 SQ
 Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 6
 AAW69294
 ID AAW69294 standard; protein; 497 AA.
 AC AAW69294;
 XX 13-NOV-1998 (first entry)
 DT
 XX Human XIAP protein.
 DE
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KM proliferative disease; IAP; therapy; cancer; human; XIAP protein.
 XX Homo sapiens.
 OS
 XX MO9835693-A2.
 EN 20-AUG-1998.
 PD
 XX 13-FEB-1998; 98MO-IB000781.
 PF
 XX 13-FEB-1997; 97US-00800929.
 PR
 XX (UYOT-) UNIV OTTAWA.
 PA
 XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 PI WPI, 1998-467164/40.
 DR N-PSDB; AAV55038.
 XX
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX
 XX Disclosure; Fig 1; 147bp; English.
 PS
 XX This sequence is the human XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 CC
 XX Sequence 497 AA:
 SQ
 Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 7
 AAY59451
 ID AAY59451 standard; protein; 497 AA.
 AC AAY59451;
 XX 24-MAR-2000 (first entry)
 DT
 XX Human XIAP protein sequence.
 DE
 XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KM transforming growth factor-beta activated kinase 1; monocyte migration;
 KM TAK1 binding protein 1; extracellular matrix protein production;
 KM cell growth inhibitor; beta-amyloid protein deposition;
 KM immunosuppression; Transforming growth factor-beta.
 XX Homo sapiens.
 OS
 XX JP11326328-A.
 PN 26-NOV-1999.
 PD
 XX 13-MAY-1998; 98JP-00130378.
 PF
 XX 13-MAY-1998; 98JP-00130378.
 PR
 XX (MATS/) MATSUMOTO K.
 PA WPI; 2000-078337/07.
 DR N-PSDB; AA248662.
 XX
 XX Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 PT
 XX Claim 3; Page 28-30; 43pp; Japanese.
 PS
 XX This sequence represents the human XIAP protein. The invention relates to
 CC a method for screening a substance inhibiting the formation of a complex
 CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
 CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
 CC protein 1 (TAB1) and a substance to be tested are contacted with each
 CC other and then the presence or formation of a complex between XIAP and
 CC TAB1 is detected. The substance can be used as a drug for extracellular
 CC matrix protein production enhancement, cell growth inhibition, monocyte
 CC migration, physiologically active substance induction, immunosuppression,
 CC and beta-amyloid protein deposition. A substance inhibiting the formation
 CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
 CC (Transforming growth factor-beta) type I and/or type II receptor is
 CC useful as a drug

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 60
 DB 265 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 8

ID AAY99985 standard; protein; 497 AA.

AC AAY99985;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis.

XX X-linked inhibitor of apoptosis; XIAP; hIAP; MHA; U45880; antisense;
 KM antiinflammatory; cytostatic; tumour.

XX Homo sapiens.

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-00392580.

XX 09-SEP-1999; 99US-00392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CP, Cowsett LM, Ackermann EJ;

XX WPI; 2000-498201/44.
 DR N-PSDB; AAA64901.

PT Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

PS Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis (the
 CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 60
 DB 265 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

DB 325 PGCKYL 330

RESULT 9

ID ABG65663 standard; protein; 497 AA.

AC ABG65663;

XX 26-AUG-2002 (first entry)

XX Human inhibitor of apoptosis, XIAP.

XX Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KM embryonic development; viral pathogenesis; autoimmune disorder;
 KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KM herpes virus infection; pox virus infection; adenovirus infection;
 KM proliferative disease.

XX Homo sapiens.

XX WO200226968-A2.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-CA001379.

XX 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Korneluk RG, Lacasse B, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

XX N-PSDB; ABX93869.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

PS Example 12; Fig 1; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer, and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 5; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 60
 DB 265 YEARIPTFGTWIYVNVKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 10
 ADB80961 ID ADB80961 standard; protein; 497 AA.

AC ADB80961;
 DT 04-DEC-2003 (first entry)

DE RING-SH complex related protein, SEQ ID NO 35.

XX RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
 KM Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIH; GTPase; E2 enzyme; tsg101;
 KM cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
 KM rhadovirus; filovirus.

XX Undenitified.

PN WO2003033646-A2.

PD 24-APR-2003.

PF 31-JUL-2002; 2002WO-US024589.

PR 31-JUL-2001; 2001US-0308958P.

XX 09-NOV-2001; 2001US-0345846P.

XX (PROT-) PROTEOLOGICS INC.

PI Greener T, Moskowitz H, Reiss Y, Alroy I;

XX WPI; 2003-393509/37.

DR N-PSDB; ADB81002.

XX New isolated protein complex comprising a RING-SH 3 polypeptide and
 PT another polypeptide, useful for detecting cells infected with a virus,
 PT and for treating viral disorders caused by retroviruses, rhadoviruses,
 PT or filoviruses.

PS Disclosure; Fig 35; 176pp; English.

XX The invention relates to a novel isolated protein complex comprising a
 CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
 CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
 CC STAM2B, VHS-UIH, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a
 CC clathrin. The novel protein complex has virucide activity and can be used
 CC to treat disorders as part of a vaccine. The protein complex and
 CC composition are useful for detecting cells infected with a virus, for
 CC identifying agents having antiviral activity, and for treating viral
 CC disorders caused by retroviruses, rhadoviruses, or filoviruses. This
 CC sequence is a protein comprising the RING-SH complex of the invention.

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 7; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAKMY 60
 DB 265 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAKMY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 11
 ADI39804

ID ADI39804 standard; protein; 497 AA.

XX ADI39804;

DT 15-APR-2004 (first entry)

DE Human inhibitor of apoptosis-like protein (ilp).

XX Inhibitor of apoptosis-like protein; ilp; ilp; apoptosis; therapy;
 KM cancer; cell immortalisation; cysteine protease; viral infection;
 KM cytoskeletal; virucide; human.

OS Homo sapiens.

PN US6511828-B1.

PD 28-JAN-2003.

PF 31-MAY-1996; 96US-00657759.

PR 31-MAY-1996; 96US-00657759.

PA (ARCH-) ARCH DEV CORP.

PI Thompson CB, Duckett CS;

DR WPI; 2003-391256/37.

XX New inhibitor of apoptosis-like protein (ilp) and polynucleotide encoding
 PT ilp, useful for inhibiting or stimulating apoptosis in target cells,
 PT treating certain cancers, or sustaining host cell survival following
 PT viral infection.

PS Claim 1; SEQ ID NO 2; 42pp; English.

XX The present invention relates to inhibitor of apoptosis (iap)-like
 CC proteins (ilp) and polynucleotides encoding such proteins. Sequences of
 CC the invention are useful for inhibiting or stimulating apoptosis in
 CC target cells or for treating certain cancers. They are also useful in the
 CC immortalisation of cells for culture, for inhibiting the activation of
 CC cysteine proteases and to sustain host cell survival following viral
 CC infection. The ilp may also be used as a marker in gel separation
 CC procedures or as a standard in protein concentration determinations. The
 CC present sequence is human inhibitor of apoptosis-like protein.

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 7; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAKMY 60
 DB 265 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAKMY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 12
 ADH74639 ID ADH74639 standard; protein; 497 AA.

XX ADH74639;

DT 15-APR-2004 (first entry)

DE Human XIAP polypeptide.

XX Biomarker; prostate neoplastic condition; inhibitor of apoptosis; IAP;
 KM XIAP; X chromosome-linked inhibitor of apoptosis; CIAP1, CIAP2;
 KM prostate cancer; human.

XX Homo sapiens.
 OS US2003224399-A1.
 XX
 XX
 PD 04-DEC-2003.
 XX
 XX 12-FEB-2003; 2003US-00366307.
 PF
 PR 12-FEB-2002; 2002US-0356956P.
 XX
 XX
 PA (REED/) REED J C.
 PA (KRAU/) KRAJEWSKI S.
 PI
 PI Reed JC, Krajewski S;
 XX
 XX WPI; 2004-141816/14.
 DR N-PSDB; ADH74638.
 XX
 PT Identifying biomarker that is diagnostic for survival of a patient with
 PT prostate neoplastic condition by measuring level of integrin associated
 PT protein in sample, and identifying correlation of the level in sample.
 PS
 PS Disclosure; SEQ ID NO 2; 42bp; English.
 XX
 XX The present invention relates to a method for identifying a biomarker
 CC that is diagnostic for the survival of patient with a prostate neoplastic
 CC condition. The method comprises measuring the level of inhibitor of
 CC apoptosis (IAP) polypeptide chosen from chosen from XIAP (X chromosome-
 CC linked inhibitor of apoptosis), CIAP1 and CIAP2 in a neoplastic prostate
 CC cell-containing sample from patients, and identifying correlation between
 CC the level of IAPs in the sample, where the correlation of an IAP with
 CC survival in the patients indicates IAP as a biomarker diagnostic. The
 CC method is useful for the prognosis of prostate neoplastic conditions such
 CC as prostate cancer. The method is efficient in determining the prognosis
 CC while the patient is still at an early stage of disease, and in
 CC monitoring the effectiveness of a particular treatment in a prostate
 CC neoplastic condition. The present sequence represents human XIAP.
 CC
 SQ Sequence 497 AA;
 Query Match 100.0%; Score 389; DB 8; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGSDGKYKCFHCGGGLTDMKPSDPPWEQHAQWY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGSDGKYKCFHCGGGLTDMKPSDPPWEQHAQWY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 13
 ID ADL70166 standard; protein; 497 AA.
 AC ADL70166;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX
 XX Human X chromosome linked inhibitor of apoptosis (XIAP).
 DE
 XX
 XX Human; inhibitor of apoptosis; IAP; XIAP; Hodgkin's disease; cytostatic;
 KM gene therapy; gene silencing.
 OS
 OS Homo sapiens.
 XX
 XX W02004017991-A1.
 PN
 XX 04-MAR-2004.
 PD
 XX

PF 18-JUL-2003; 2003WO-EP007889.
 XX
 XX 13-AUG-2002; 2002DE-01037139.
 XX
 XX
 PA (CELL-) CELL CENT COLOGNE GMBH.
 XX
 XX Kroenke M, Kaashkar H, Hamilton-Dutoit SJ, Jurgensmeier JM;
 PI
 PI WPI; 2004-226745/21.
 DR N-PSDB; ADL70165.
 XX
 XX
 PT Using inhibitors of apoptosis-inhibitor for preparation of pharmaceutical
 PT composition for treatment of Hodgkin's lymphomas.
 PS
 PS Claim 11; SEQ ID NO 2; 61bp; English.
 XX
 XX The present sequence is the protein sequence of human X chromosome linked
 CC inhibitor of apoptosis (XIAP). The invention is based on the discovery
 CC that IAPs, e.g. XIAP, are constitutively overexpressed in both Hodgkin's
 CC lymphoma (HL)-derived B-cell lines and in primary HL tissues, and that in
 CC B-cell lines they are associated with and inhibit in particular caspase-
 CC 3. Based on this finding, the invention provides a new therapy of HL,
 CC which is based on inhibitors of IAPs, especially XIAP, that reduce or
 CC eliminate the caspase inhibiting activity. The approach leads to the
 CC restoration of apoptotic mechanisms, which result in an increased number
 CC of cell death events in malignant HL cells. Since IAPs, in particular
 CC XIAP, are not overexpressed in normal tissues, the approach provides a
 CC selective therapy for HL. Suitable IAP inhibitors include molecules that
 CC reduce the level of IAP mRNA, reduce the level of the IAP, inhibit the
 CC binding of the IAP to a caspase or reduce the biological activity of the
 CC IAP, e.g. an antisense nucleic acid, short interfering RNA (siRNA),
 CC ribozyme, anti-IAP antibody, anti-IAP aptamer, small molecule, peptide or
 CC peptidomimetic. Diagnostic methods for the detection of HL using IAP
 CC specific agents are also provided.
 CC
 SQ Sequence 497 AA;
 Query Match 100.0%; Score 389; DB 8; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGSDGKYKCFHCGGGLTDMKPSDPPWEQHAQWY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGSDGKYKCFHCGGGLTDMKPSDPPWEQHAQWY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 14
 ID ADP23982 standard; protein; 497 AA.
 AC ADP23982;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 XX
 XX PRO polypeptide SEQ ID NO:1160.
 DE
 XX
 XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
 OS
 OS Unidentified.
 XX
 XX W02004041170-A2.
 PN
 XX 21-MAY-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034312.
 PF
 XX 01-NOV-2002; 2002US-0423394P.
 PR


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XX AC AAW19745;
XX
XX 16-SEP-1997 (first entry)
DT
XX
XX Mouse inhibitor of apoptosis protein homologue MHA.
DE
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHA;
XX degenerative disease; infectious disease; autoimmune disease; cancer;
XX therapy; diagnosis.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH Region 26..93
FT /label= BIR
FT Region 163..230
FT /label= BIR
FT Region 264..330
FT /label= BIR
FT Region 448..485
FT /label= RING_finger
XX
XX W09723501-A1.
XX
XX 03-JUL-1997.
XX
XX 20-DEC-1996; 96MO-AU000827.
XX
XX 22-DEC-1995; 95AU-00007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI; 1997-350966/32.
XX
XX N-PSDB; AAT72710.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
PT modulate apoptosis for treatment of degenerative, infectious or
PT auto-immune diseases and cancer.
XX
XX Claim 7; Page 44-47; 136pp; English.
XX
XX Mammalian IAP homologue A (MHA) (AAW19745) is a murine homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence
CC was deduced from a cDNA clone (see also AAT72710) isolated from a mouse
CC liver cDNA library on the basis of homology to Oryza pseudotsugata
CC polyhedrosis virus IAP BIR and RING finger amino acid motifs (see also
CC AAW19744). IAP homologues (see also AAW19746-52) and their derivatives
CC and chemical analogues can be used in methods for modulating apoptosis in
CC animal cells, specifically for treatment, by inhibition, of degenerative
CC and infectious disease or, by promotion, of cancer and autoimmune disease
XX
XX Sequence 496 AA;
SQ
Query Match 94.6%; Score 368; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 6.3e-36;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDWKPSPDPMEQHAQMY 60
Db 264 YEARIIVFGTWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDWKPSPDPMEQHAQMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

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AC AAW19584;
XX
XX 02-SEP-1997 (first entry)
DT
XX
XX Mouse apoptosis inhibitor M-XIAP.
DE
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
XX HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
XX myocardial infarction; stroke; reperfusion injury;
XX toxin-induced liver disease; gene therapy; diagnosis.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH Domain 26..93
FT /label= BIR-1
FT Domain 163..230
FT /label= BIR-2
FT Domain 264..329
FT /label= BIR-3
FT Domain 438..483
FT /label= RING_zinc_finger
XX
XX W09706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96MO-IB001022.
XX
XX 04-AUG-1995; 95US-00511485.
XX
XX 22-DEC-1995; 95US-00576956.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Korneluk RG, Mackenzie AB, Baird S, Liston P;
XX
XX WPI; 1997-154262/14.
XX
XX N-PSDB; AAT70839.
XX
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
XX Claim 27; Page 79-80; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP) and which are characterized by the presence of a ring
CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
CC was deduced from the m-xiap gene (AAT70839) isolated from a mouse embryo
CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
CC vitro or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease
XX
XX Sequence 496 AA;
SQ
Query Match 94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 1.1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDWKPSPDPMEQHAQMY 60
Db 264 YEARIIVFGTWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDWKPSPDPMEQHAQMY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

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RESULT 17
AAW19584
ID AAW19584 standard; protein; 496 AA.
XX

RESULT 18
AAW69297 standard; protein; 496 AA.
AC AAW69297;
XX
DT 13-NOV-1998 (first entry)
XX
DE Murine XIAP protein.
XX
KM Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX
OS Mus sp.
XX WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneljuk R, Mackenzie AE, Iliston P, Baird S, Tsang B, Pratt C;
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55041.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Disclosure; Fig 4; 147pp; English.
XX
CC This sequence is the murine XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX
SQ Sequence 496 AA;
Query Match 94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 1,1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARITFTGWTISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 60
DB 264 YEARITFTGWTISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 19
ABG65666 standard; protein; 496 AA.
XX
AC ABG65666;
XX

DT 26-AUG-2002 (first entry)
XX
XX Mouse inhibitor of apoptosis, XIAP.
XX
KM Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KM embryonic development; viral pathogenesis; autoimmune disorder;
KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KM herpes virus infection; pox virus infection; adenovirus infection;
KM proliferative disease.
XX
OS Mus sp.
XX WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CN001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneljuk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI; 2002-479562/51.
DR N-PSDB; ABK93872.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 4; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (1) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence
XX
SQ Sequence 496 AA;
Query Match 94.1%; Score 366; DB 5; Length 496;
Best Local Similarity 95.5%; Pred. No. 1,1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARITFTGWTISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 60
DB 264 YEARITFTGWTISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 20
ADB61828 standard; protein; 66 AA.
XX
ID ADB61828
XX

AC AD861828;
 DT 04-DEC-2003 (first entry)
 XX Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
 DE
 XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KM autoimmune disorder; neurodegenerative disease; apoptotic response;
 KM systemic lupus erythematosus; multiple sclerosis; viral infection;
 KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KM HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KM caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
 KM cervical cancer; uterine cancer; testicular cancer;
 KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KM Wilm's tumour; BIR 3 domain; mouse; murine.
 XX
 OS Mus sp.
 XX
 PN WO2003040172-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 12-NOV-2002; 2002MO-CA001738.
 XX
 PR 09-NOV-2001; 2001US-0332300P.
 PR 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Boudreauc A, Korneluk RG, La Casse E, Liston P;
 DR WPI; 2003-513532/48.
 XX
 PT polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1B; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC that inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.

Query Match	90.5%	Score 352	DB 7	Length 66
Best Local Similarity	92.4%	Pred. No. 5	5e-35	
Matches 61	Conservative 1	Mismatches 4	Indels 0	Gaps 0
QY	1	YEARIFTEGTWISYVNKEQLADAPGAYALGEGNKVRCFCGGSLTDMKPSDEDEQHAKKY	60	

Db 1 YEARIIVTFGWTSSVINKQLARAGFTALGEGDVKCFHCGGGLTDMKPSBEDPMDQIAKCY 60

QY 61 PGCKYL 66
| | | | |

Db 61 PGCKYL 66

RESULT 21
ABP72157
ID ABP72157 standard; protein; 496 AA

DT 22-APR-2003 (first entry)

Mouse inhibitor of apoptosis protein MIAP3.

KW Inhibitor of apoptosis; MIAF3; mouse; apoptosis; cancer; leukaemia;
 KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy

OS MUB 8P.

PN WO2003004606-A2

PD 16-JAN-2003

PR 03-JUL-2002; 2002WO-US021002.

PR 03-JUL-2001; 2001US-00898158.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Troy CM, Shelanski ML;

DR WPI; 2003-210351/20.

XX

PT treating cancer, neurodegenerative disorder or cardiomyopathy.

PS Disclosure; Fig 15A; 124pp; English.

CC The present sequence is the protein sequence of murine inhibitor of
CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as
CC an antisense oligonucleotide, which specifically hybridises to a nucleic
CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
CC death comprises contacting the cell with the nucleic acid under
CC conditions permitting the nucleic acid to enter the cell, especially the
CC use of a vector, liposome, or a mechanical or electrical means. The
CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
CC cell carcinoma and squamous cell carcinoma (all claimed)

SQ Sequence 496 AA;

Query Match	90.5%	Score 352	DB 6	Length 496
Best Local Similarly	92.4%	Pred. No. 5	6e-34	
Matches 61	Conservative 1	Mismatches 4	Indels 0	Gaps 0

```
OY      1 YEARIFTGWTIYSVNKEQLARAGFYALGBEDGVKVCFHCGGGITDVKPSSEDPWEQHAHW 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      264 YEARIVTFGWTTSSVNKEQLARAGFYALGBEDGVKVCFHCGGGITDVKPSEDPPVDHACY 322
```

61 PGCKYL 66 QY

Db 324 PGCKYL 329

RESULT 22

ID ADB61820 standard; protein; 66 AA

XX Sequence 236 AA;
SQ

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 9.7e-34;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDEPMEQHAKEY 60
DB 4 YEARIITFGTWISVYNKEQLARAGFYALGEGDKVKCFHCGGGLANMKPKEDPMEQHAKEY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 24
AAE00365
ID AAE00365 standard; protein, 236 AA.
XX
AC AAE00365;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human IAP-1like protein-2 (ILP-2) with TGFbetar modulating activity.
XX
KM Human; inhibitor of apoptosis; IAP-1like protein-2; ILP-2;
KM chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
KM TGFbetar; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KM cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KM T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KM retinal degeneration; hyperferitinaemia-cataract syndrome; cancer;
KM autoimmune disease; diabetes; multiple sclerosis; cytoskeletal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 7..70
FT /label= BIR domain
FT /note= "Baculovirus iap repeat"
FT Domain 188..223
FT /label= RING_finger_domain
XX
PN WO200123568-A2.
XX
PD 05-APR-2001.
XX
PP 29-SEP-2000; 2000WO-US026735.
XX
PR 30-SEP-1999; 99US-0157169P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Duckett C, Mir SS;
XX
DR WPI; 2001-258135/26.
DR N-PSDB; AAD03581.
XX
PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis.
XX
PS Claim 1; Fig 2; 108pp; English.
XX
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC (ILP-2). The hILP-2 gene is located on chromosome 19q13.3-q13.4. ILP-2
CC comprises a single amino-terminal domain known as baculovirus iap repeat
CC (BIR), followed by a spacer region and a carboxy-terminal ring finger
CC domain. It interacts with transforming growth factor beta receptor
CC (TGFbetar) and modulates TGFbetar activity. It also potentially inhibits
CC apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It
CC also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in

CC the area of genetic testing for predisposition to diseases, such as cone-
CC rod retinal dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell
CC acute lymphoblastic leukaemia, colorectal cancer and hyperferitinaemia-
CC cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also
CC used in the treatment of diseases associated with abnormal apoptosis such
CC as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
CC neurodegenerative diseases including retinal degeneration. The ILP-2 gene
CC is also used in gene therapy for treating patients suffering from ILP-2
CC gene deletions or mutations
XX

SQ Sequence 236 AA;
Query Match 89.2%; Score 347; DB 4; Length 236;
Best Local Similarity 84.8%; Pred. No. 9.7e-34;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDEPMEQHAKEY 60
DB 4 YEARIITFGTWISVYNKEQLARAGFYALGEGDKVKCFHCGGGLANMKPKEDPMEQHAKEY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 25
AAU75066
ID AAU75066 standard; protein, 236 AA.
XX
AC AAU75066;
XX
DT 23-APR-2002 (first entry)
XX
DE Human testes specific inhibitor of apoptosis (TIAP) protein.
XX
KM TIAP; apoptosis; testes specific inhibitor of apoptosis; human;
KM apoptotic; cytostatic; anti-infertility; contraceptive;
KM chromosome 12q22-23; transgenic animal; antibody; immunogen;
KM testicular cell; testicular cancer; cancer; male infertility;
KM male birth control; XIAP.
XX
OS Homo sapiens.
XX
PN US6331412-B1.
XX
PD 18-DEC-2001.
XX
PP 29-JAN-1999; 99US-00239867.
XX
PR 29-JAN-1998; 98US-0073001P.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Lagace M;
XX
DR WPI; 2002-105275/14.
DR N-PSDB; ABK13197.
XX
PT Nucleic acids encoding a testis specific apoptosis inhibitor protein
PT (TIAP) useful for treating testicular cancers, cancers in non-testicular
PT tissues, male infertility, and for achieving male birth control.
XX
PS Example 4; Fig 4B; 29pp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a TIAP polypeptide (testes-specific inhibitor of apoptosis) protein. This
CC gene is a homologue of the X-linked XIAP gene and is located on
CC chromosome 12q22-23. The nucleotide and protein sequences of the
CC invention and vectors containing these sequences may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC be used to express the TIAP protein by recombinant methods. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate

CC TIAP expression. The nucleotide sequence, may also be used to design DNA
 CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
 CC detect and quantify the presence of similar nucleic acid sequences in
 CC samples, to identify patients who may be in need of restorative therapy.
 CC Through the production of transgenic animals and cells, the sequences may
 CC also be used to study the expression and function of TIAP proteins and
 CC their role in metabolism. The TIAP polypeptides may be used to produce
 CC antibodies against TIAP and maybe used to identify modulators (agonists
 CC or antagonists) of TIAP expression and activity. An anti-TIAP antibody
 CC or antagonist may also be used to down-regulate TIAP expression and
 CC activity. The reagents may be used in this way for the treatment of
 CC excessive or insufficient apoptosis, particularly in testicular cells. In
 CC particular they are useful in diagnosing and treating testicular cancers,
 CC cancers in non-testicular tissues, male infertility, and for achieving
 CC male birth control. The present sequence represents the human TIAP
 CC protein sequence of the invention

XX Sequence 236 AA;

Query Match 89.2%; Score 347; DB 5; Length 236;

Best Local Similarity 84.8%; Pred. No. 9,7e-34; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKMY 60
 DB 4 YEARIPTFGTWIYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKMY 63

QY 61 PGCKYTL 66
 DB 64 PGCKYTL 69

RESULT 26

ABG32417 standard; protein; 236 AA.

XX ABG32417;

XX 15-NOV-2002 (first entry)

DE Inhibitor of apoptosis protein, TIAP.

XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;

KW fertility; testicular cancer; male infertility; male birth control.

XX Mammalia.

OS Key Location/Qualifiers

FT Misc-difference 1 /note="Encoded by run; start codon is illegible in
 FT specification"

XX US2002086409-A1.

XX 04-JUL-2002.

XX 18-DEC-2001; 2001US-00024433.

XX 29-JAN-1998; 98US-0073001P.

PR 29-JAN-1999; 99US-00239867.

XX (KORN/) KORNELUK R G.

PA (LAGA/) LAGACE M.

PI Korneluk RG, Lagace M;

XX WPI; 2002-642245/69.

DR N-PSDB; ABS52802.

XX Novel polypeptide, a member of inhibitor of apoptosis family of proteins
 PT that is expressed in testes useful for modulating apoptosis in cells,
 PT particular cells involved in male fertility.

PS Example 3; Fig 4B; 24pp; English.

XX A substantially pure TIAP polypeptide (1), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (1) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (1) is useful for increasing apoptosis in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (1) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the amino
 CC acid sequence of TIAP

XX Sequence 236 AA;

Query Match 89.2%; Score 347; DB 5; Length 236;

Best Local Similarity 84.8%; Pred. No. 9,7e-34; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKMY 60
 DB 4 YEARIPTFGTWIYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKMY 63

QY 61 PGCKYTL 66
 DB 64 PGCKYTL 69

RESULT 27

AAU75747 standard; protein; 464 AA.

XX AAU75747;

XX 08-MAY-2002 (first entry)

DE Human Inhibitor of apoptosis protein 7 (IAPL7) protein.

XX Human; inhibitor of apoptosis 7; IAPL7; cytostatic; antiapoptotic; IAP;

KW apoptosis; V-Rel; cancer; NF-kappaB; chromosome 19; vaccine;

KW gene therapy; hyperproliferative disease; transgenic animal; antibody.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Region 1..133 /note="This sequence is specifically claimed in claim 1
 FT of the specification and is encoded by the nucleic acid
 FT represented in ABK14678"

XX WO200210381-A1.

XX 07-FEB-2002.

XX 18-JUL-2001; 2001WO-EP008287.

XX 28-JUL-2000; 2000EP-00116452.

XX (MERE) MERCK PATENT GMBH.

XX Hentsch B;

XX WPI; 2002-188741/24.

DR P-PSDB; ABK14677.

XX New inhibitor of apoptosis proteins and polynucleotides useful in
 PT vaccines for inducing an immune response against hyperproliferative
 PT diseases e.g. cancer.

XX Claim 1; Page 35-36; 41pp; English.

XX This invention relates to the nucleic acid and protein sequences of a

CC novel inhibitor apoptosis protein (IAP17) polypeptide. These sequences
 CC have homology to the IAP (inhibitors of apoptosis) gene family which are
 CC thought to inhibit proteases by regulating the anti-apoptotic activity of
 CC the V-Rel and NF-kappaB family of transcription factors. The gene for
 CC IAP17 is located on human chromosome 19. The nucleic acids of the
 CC invention are useful for screening to identify compounds that stimulate
 CC or inhibit the function or level of IAP17, where the identified compounds
 CC are useful for treating hyper-proliferative diseases such as cancer. The
 CC protein sequences may also be used to identify membrane bound or soluble
 CC receptors of IAP17 by standard receptor binding techniques. Nucleic acids
 CC encoding IAP17, may be used as hybridisation probes for cDNA and genomic
 CC DNA, or as primers for nucleic acid amplification reaction and the
 CC primers and probes may also be used to isolate full-length cDNAs and
 CC genomic clones encoding IAP17. The nucleic acid sequences are useful as
 CC diagnostic reagents for diagnosing a disease or a susceptibility to a
 CC disease by detecting mutations in the associated gene. The nucleic acid
 CC sequence is useful for chromosome localisation and tissue expression
 CC studies and is also useful for producing transgenic animals. The IAP17
 CC protein sequence may also be used to generate an anti-IAP17 antibody
 CC which is useful in screening methods for detecting the effect of added
 CC compounds on the production of mRNA and protein in cells. The sequences
 CC of the invention are also useful as vaccines for inducing an
 CC immunological response in a mammal. The present sequence represents the
 CC human inhibitor of apoptosis 7 (IAP7) protein of the invention
 CC
 SQ Sequence 464 AA;

Query Match 89.2%; Score 347; DB 5; Length 464;
 Best Local Similarity 84.8%; Pred. No. 2.1e-33;
 Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMEQHAQMY 60
 DB 232 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMEQHAQMY 291

QY 61 PGCKYL 66
 DB 292 PGCKYL 297

RESULT 28

ADR44576 ADR44576 standard; protein; 87 AA.

AC ADR44576;

DT 18-NOV-2004 (first entry)

DE X-IAP BIR3 domain.

XX BIR domain binding oligopeptide; BIR oligopeptide;
 KW melanoma inhibitor of apoptosis; ML-IAP; caspase inhibition; apoptosis;
 KW cancer; IAP antagonist; baculovirus IAP repeat domain; BIR domain;
 KW melanoma; breast cancer; colorectal cancer; lung cancer; ovarian cancer;
 KW central nervous system cancer; liver cancer; bladder cancer;
 KW pancreatic cancer; cervical cancer; leukaemia; fruit fly; sickle;
 KW small subunit; N-terminal; X-IAP.

OS Unidentified.

PN US2004171554-A1.

PD 02-SEP-2004.

PF 07-FEB-2003; 2003US-00364645.

PR 07-FEB-2003; 2003US-00364645.

XX (GETH) GENENTECH INC.

PA Deebayes K, Fairbrother W, Flygare J, Franklin MC, Fischer S,
 PI Vucic D;

DR WPI; 2004-651687/63.

XX New isolated BIR domain binding (BDB) oligopeptide that specifically
 PT binds melanoma inhibitor of apoptosis (ML-IAP) and releases the
 PT inhibitory effect that ML-IAP has on caspase activity, useful for
 PT increasing apoptosis in cells.

XX Example 10; Fig 5; 50pp; English.

XX The invention describes an isolated BIR domain binding (BDB) oligopeptide
 CC that specifically binds melanoma inhibitor of apoptosis (ML-IAP) and
 CC releases the inhibitory effect that ML-IAP has on caspase activity. Also
 CC described are: a method of increasing apoptosis in a cell comprising
 CC contacting the cell with the oligopeptide, where the apoptosis is
 CC increased; an article of manufacture comprising a container; the
 CC composition of matter contained within the container; and a label affixed
 CC to the container, or a package insert included with the container,
 CC referring to the use of the composition of matter for the therapeutic
 CC treatment of or the diagnostic detection of a cancer; a method of
 CC screening antagonists of IAP polypeptides comprising co-crystallising the
 CC potential antagonist with the Baculovirus IAP repeat (BIR) domain of an
 CC ML-IAP polypeptide to form a co-crystalline structure and determining if
 CC the potential antagonist binds to the BIR domain; determining whether the
 CC antagonist increases apoptosis in cells relative to antagonist untreated
 CC cells; a method of screening antagonists of an ML-IAP polypeptide
 CC comprising co-crystallising the potential antagonist with the BIR domain
 CC of an ML-IAP polypeptide to form a co-crystalline structure and
 CC determining if the potential antagonist binds to the BIR domain, and
 CC where binding occurs if there is at least one contact between a specific
 CC amino acid residue of a given patch and the candidate molecule that is
 CC less than or equal to 2.8 angstroms in the co-crystalline structure. The
 CC oligopeptide and composition of matter are useful for increasing
 CC apoptosis in cells, preferably cancer cells such as a melanoma cell, a
 CC breast cancer cell, a colorectal cancer cell, a lung cancer cell, an
 CC ovarian cancer cell, a central nervous system cancer cell, a liver cancer
 CC cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer
 CC cell, and a leukaemia cell. This is the amino acid sequence of IAP BIR
 CC domain associated with the selection of BIR domain binding oligopeptides.
 CC
 SQ Sequence 87 AA;

Query Match 88.0%; Score 342.5; DB 8; Length 87;
 Best Local Similarity 90.9%; Pred. No. 1.1e-33;
 Matches 60; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMEQHAQMY 60
 DB 9 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMEQHAQMY 67

QY 61 PGCKYL 66
 DB 68 PGCKYL 73

RESULT 29

AAE00366 AAE00366 standard; protein; 236 AA.

AC AAE00366;

DT 19-JUN-2001 (first entry)

DE Chimpanzee IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.

XX Chimpanzee; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
 KW transforming growth factor beta receptor; TGFbetaR;
 KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
 KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
 KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 KW retinal degeneration; hyperferritinemia-cataract syndrome; cancer;
 KW autoimmune disease; diabetes; multiple sclerosis; cytostatic.

OS Pan troglodytes.

XX Gorilla IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
 DE
 XX
 XX transforming growth factor beta receptor; TGFbetaR; cytoskeletal;
 KM
 KM c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
 KM
 KM cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
 KM
 KM T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 KM
 KM retinal degeneration; hyperferitinaemia-cataract syndrome; cancer;
 KM
 KM autoimmune disease; diabetes; multiple sclerosis.
 XX
 OS Gorilla gorilla.
 XX
 PN MO200123568-A2.
 XX
 XX 05-APR-2001.
 PD
 XX 29-SEP-2000; 2000MO-US026735.
 PF
 XX 30-SEP-1999; 99US-0157169P.
 PR
 XX (USSS) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Duckett C, Mir SS;
 PI
 XX WPI; 2001-258135/26.
 DR
 XX N-PSDB; AAD03583.
 XX
 PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
 PT transforming growth factor beta receptor modulating activity, and the
 PT nucleic acids that encode them, useful for treating, e.g. diabetes and
 PT multiple sclerosis.
 PS Claim 1; Fig 2; 108pp; English.
 XX
 XX The present sequence is gorilla inhibitor of apoptosis (IAP)-like protein
 CC -2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain known as
 CC baculovirus iap repeat (BIR), followed by a spacer region and a carboxy-
 CC terminal ring finger domain. It interacts with transforming growth factor
 CC beta receptor (TGFbetaR) and modulates TGFbetaR activity. It also
 CC potentially inhibits apoptosis induced by overexpression of Bax or by
 CC Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
 CC activity. ILP-2 is used in the area of genetic testing for predisposition
 CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
 CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
 CC and hyperferitinaemia-cataract syndrome owing to an ILP-2 deletion or
 CC mutation. The ILP is also used in the treatment of diseases associated
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
 CC diabetes and multiple sclerosis and neurodegenerative diseases including
 CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
 CC treating patients suffering from ILP-2 gene deletions or mutations
 CC
 XX
 SQ Sequence 236 AA;
 Query Match 86.9%; Score 338; DB 4; Length 236;
 Best Local Similarity 81.8%; Pred. No. 1.2e-32;
 Matches 54; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEALIFPGTWTIVSVNKQLARAFYALGSDGYKCFHCGGGLTDMKPSDDPEQHAQMY 60
 DB 4 YEALIFPGTWTIVSVNKQLARAFYALGSDGYKCFHCGGGLTDMKPSDDPEQHAQMY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69
 RESULT 32
 ADB61832
 ID ADB61832 standard; protein; 57 AA.
 XX
 AC ADB61832;
 XX

DT 04-DEC-2003 (first entry)
 XX
 DE Unidentified inhibitor of apoptosis (IAP) protein IAP BIR3 domain.
 XX
 KM baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KM
 KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KM
 KM autoimmune disorder; neurodegenerative disease; apoptotic response;
 KM
 KM systemic lupus erythematosus; multiple sclerosis; viral infection;
 KM
 KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KM
 KM XIAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KM
 KM caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
 KM
 KM cervical cancer; uterine cancer; testicular cancer;
 KM
 KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KM
 KM Wilms' tumour; BIR 3 domain.
 XX
 OS Unidentified.
 XX
 PN MO2003040172-A2.
 PD
 XX 15-MAY-2003.
 PF
 XX 12-NOV-2002; 2002MO-CA001738.
 PR
 XX 09-NOV-2001; 2001US-0332300P.
 PR
 XX 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 PI
 XX Boudreaux A, Korneluk RG, La Casse E, Liston P;
 PT WPI; 2003-513532/48.
 DR
 XX
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating a
 PT cancer and other neoplasms.
 PT
 PS Disclosure; Fig 1b; 53pp; English.
 XX
 XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the an unidentified inhibitor of apoptosis (IAP) protein IAP BIR3
 CC domain which was used to demonstrate homology to human IAP protein BIR
 CC domains to which the peptides of the invention are targeted to bind.
 CC
 XX
 SQ Sequence 57 AA;
 Query Match 82.8%; Score 322; DB 7; Length 57;
 Best Local Similarity 94.6%; Pred. No. 2.1e-31;
 Matches 53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 11 WTSVKNKEQLARAFYALGSDGYKCFHCGGGLTDMKPSDDPEQHAQMYPGCKYL 66
 DB 2 WTSVKNKEQLARAFYALGSDGYKCFHCGGGLTDMKPSDDPEQHAQMYPGCKYL 57


```
RESULT 33
AD139821
ID AD139821 standard; protein; 53 AA.
AC
XX AD139821;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NAIp BIRa region #1.
XX
XX Inhibitor of apoptosis-like protein; iap; iip; apoptosis; therapy;
XX cancer; cell immortalisation; cytosine protease; viral infection;
XX cytosolic; virucide; baculovirus iap-like repeat; BIR; human;
XX neural apoptosis inhibitory protein; NAIp.
XX
XX Homo sapiens.
XX
XX US6511828-B1.
XX
XX 28-JAN-2003.
XX
XX 31-MAY-1996; 96US-00657759.
XX
XX 31-MAY-1996; 96US-00657759.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Thompson CB, Duckett CS;
XX
XX WPI; 2003-391256/37.
XX
XX New inhibitor of apoptosis-like protein (iip) and polynucleotide encoding
XX iip, useful for inhibiting or stimulating apoptosis in target cells,
XX treating certain cancers, or sustaining host cell survival following
XX viral infection.
XX
XX Example 2; SEQ ID NO 19; 42pp; English.
XX
XX The present invention relates to inhibitor of apoptosis (iap)-like
XX proteins (iip) and polynucleotides encoding such proteins. Sequences of
XX the invention are useful for inhibiting or stimulating apoptosis in
XX target cells or for treating certain cancers. They are also useful in the
XX immortalisation of cells for culture, for inhibiting the activation of
XX cytosine proteases and to sustain host cell survival following viral
XX infection. The iip may also be used as a marker in gel separation
XX procedures or as a standard in protein concentration determinations. The
XX present sequence is human neural apoptosis inhibitory protein (NAIP)
XX baculovirus iap-like repeat (BIR) region.
XX
XX Sequence 53 AA;
XX
XX Query Match 75.8%; Score 295; DB 7; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-28;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 18 EQIARAGFYALGSDGVKCFHCGGGLTDMKPSDPMWQHAKWPGCKYL 66
XX |||||
XX 1 EQIARAGFYALGSDGVKCFHCGGGLTDMKPSDPMWQHAKWPGCKYL 49
XX
XX RESULT 34
XX ADB61829 standard; protein; 66 AA.
XX
XX ADB61829;
XX
XX 04-DEC-2003 (first entry)
XX
XX Chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
XX apoptosis pathway; embryonic development; viral pathogenesis; cancer;
```

```
XX autoimmune disorder; neurodegenerative disease; apoptotic response;
XX systemic lupus erythematosus; multiple sclerosis; viral infection;
XX herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
XX H1AP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
XX caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
XX cervical cancer; uterine cancer; testicular cancer;
XX small cell lung carcinoma; uterine cancer; renal cell carcinoma;
XX Wilms tumour; BIR 3 domain; chicken.
XX
XX Gallus gallus.
XX
XX WO2003040172-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002WO-CA001738.
XX
XX 09-NOV-2001; 2001US-0332300P.
XX
XX 08-APR-2002; 2002US-0370934P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Boudreau A, Korneluk RG, La Casse E, Liston P;
XX
XX WPI; 2003-513532/48.
XX
XX Polypeptide capable of forming a complex with a polypeptide comprising a
XX baculovirus inhibitor of apoptosis repeat domain useful for treating a
XX cancer and other neoplasms.
XX
XX Disclosure; Fig 1B; 53pp; English.
XX
XX This invention relates to a substantially pure polypeptide having a
XX length of less than 100 amino acids and capable of forming a complex with
XX a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
XX (BIR) domain. The apoptosis pathway is known to play a critical role in
XX embryonic development, viral pathogenesis, cancer, autoimmune disorders
XX and neurodegenerative diseases. The failure of the apoptotic response has
XX been implicated in the development of cancer, autoimmune disorders (for
XX example systemic lupus erythematosus and multiple sclerosis) and viral
XX infections (including herpes virus, poxvirus and adenovirus. The
XX inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
XX more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1
XX (CIAP2) and H1AP2 (CIAP1) all possess three BIR domains and carboxy
XX terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
XX -9 which are proteases involved in the initiation of apoptosis. Compounds
XX through inhibit the activity of IAPs may therefore have cytostatic activity
XX through the enhancement of apoptosis. The polypeptides of the invention
XX are candidate peptide ligands for binding to the BIR domain of IAPs. They
XX may be useful for the treatment of cancer and other neoplasms, such as
XX leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
XX cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
XX and Wilms tumour, and for enhancing apoptosis. The present sequence is
XX that of the chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
XX which was used to demonstrate homology to human IAP protein BIR domains
XX to which the peptides of the invention are targeted to bind.
XX
XX Sequence 66 AA;
XX
XX Query Match 73.8%; Score 287; DB 7; Length 66;
XX Best Local Similarity 71.2%; Pred. No. 4.5e-27;
XX Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
XX
XX 1 YEARIPTFGTWIYSVKNQOLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMWQHAKWY 60
XX |||||
XX 1 YERRIOTPLAWIYPVNKEHLARAGFYSTNGSDHVCYFHCSSGLQEWKENEDWDQHAKWF 60
XX |||||
XX 61 PGCKYL 66
XX |||||
XX 61 PGCKFL 66
XX
XX RESULT 35
```


ADK34975	ADK34975 standard; protein; 151 AA.
ID	ADK34975
XX	
AC	ADK34975;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Novel human polypeptide SegID7057.
XX	
KM	antiarthritic; antiparkinsonian; neuroprotective; nootropic;
KM	immunosuppressive; cytostatic; antipsoriatic; antiinflammatory;
KM	antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
KM	arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
KM	psoriasis; inflammatory bowel disease; infection; bacteria; virus;
XX	fungus; parasite; human.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Misc-difference 1..151
FT	/label= OTHER
FT	/note= "OTHER= All Xaa's in this sequence are unknown
FT	amino acids or the site of a stop codon within the DNA
FT	sequence"
XX	
PN	WO200216439-A2.
XX	
PD	28-FEB-2002.
XX	
PF	05-MAR-2001; 2001WO-US004941.
XX	
PR	07-MAR-2000; 2000US-00519705.
PR	19-MAY-2000; 2000US-00574454.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
F1	Tang YT, Liu C, Drmanac RT;
DR	WPI; 2002-280918/32.
XX	
PT	Isolated polynucleotide encoding bone marrow derived polypeptides useful
PT	for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
PT	disease, and inflammatory bowel disease.
XX	
PS	Claim 20; SEQ ID NO 7057; 504pp; English.
XX	
CC	This invention relates to a novel isolated polynucleotide comprising a
CC	nucleotide sequence selected from one of 1680 sequences, a mature protein
CC	coding portion of them, an active domain of them and their complementary
CC	sequences. The invention may be useful for the production of compounds
CC	with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
CC	immunosuppressive, cytostatic, antipsoriatic, antiinflammatory,
CC	antibacterial, antiviral, antifungal or antiparasitic activity. In
CC	addition, the disclosed sequences may be useful for gene therapy. The
CC	polypeptides or their antibodies are useful for treating many diseases
CC	such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
CC	psoriasis, inflammatory bowel disease and infections caused by bacteria,
CC	viruses, fungi or parasites. The present sequence is that of a human
CC	polypeptide of the invention.
XX	
XX	
XX	Sequence 151 AA;
XX	

Query Match	70.2%	Score 273;	DB 5;	Length 151;
Best Local Similarity	74.2%	Pred. No. 5,9e-25;		
Matches	49;	Conservative	4;	Mismatches 13; Indels 0; Gaps 0.
Qy	1	YEARIPTFGTWTYSYNKEQLARAGFYALGEGDKVCKFHGGGLTDWKSSEDPWEQHAKMY	60	
Db	6	YEAQIITIGMMWYSYNKOOHAGAEFYALGKGDKVCKFCGGRRLTDWKEIDIEHREPHAKMY	65	
Qy	61	PGCKYL	66	
Db	66	PRCKYL	71	

RESULT 36
 ADB61830
 ID ADB61830 standard; protein, 52 AA.
 XX
 AC ADB61830;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Bovine inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
 XX
 KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW H1A1; cIAP2; H1AP2; cIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW small cell cancer; uterine cancer; testicular cancer;
 KW Wilms' tumour; BIR 3 domain; bovine; cow.
 KM
 OS Bos taurus.
 XX
 PN WO2003040172-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 12-NOV-2002; 2002WO-CA001738.
 XX
 PR 09-NOV-2001; 2001US-0332300P.
 PR 08-APR-2002; 2002US-0370934P.
 XX
 PA (ABGEA-) ABGEA THERAPEUTICS INC.
 XX
 PI Boudreau A, Korneluk RG, La Casse E, Liston P;
 DR WPI; 2003-513532/48.
 XX
 PT polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1B; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1A1
 CC (cIAP2) and H1AP2 (cIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemia, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the bovine inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 52 AA;

PS Disclosure, Fig 1B, 53pp, English.
XX
XX This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAI1
CC (cIAP2) and HAI2 (cIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the bovine inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.
XX
XX Sequence 52 AA;

CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HAPI2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein HAPI BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

SO Sequence 68 AA;

Query Match 54.2%; Score 211; DB 7; Length 68;
 Best Local Similarity 57.4%; Pred. No. 8.2e-18;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTGFWIVS--VNKEQLARAGFYALGSDKVKCFHCGGLTDMKSEDPWEQHA 58
 DB 1 HAARFKTFPMWPSVLVNPQLASAGFYVGNSDVVCFCDDGGLRCWESGDDPWVQHA 60
 QY 59 WYPCCKYL 66
 DB 61 WFPRCXYL 68

RESULT 39

ADO26592 ID ADO26592 standard; protein; 442 AA.

AC ADO26592;

DT 01-JUL-2004 (first entry)

XX Human APl2.

XX Chromosome translocation; malignancy;
 KM mucosa-associated lymphoid tissue-lymphoma associated translocation;
 KM MLT; MLT; primary cell transformation; apoptosis inhibitor 2; APl2;
 KM tumour; cytostatic; human.

XX Homo sapiens.

XX US6689875-B1.

XX 10-FEB-2004.

XX 26-MAY-2000; 2000US-00579692.

XX 09-JUN-1999; 99US-0138834P.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Dierlamm J, Baens M, Marijnen P;

XX WPI; 2004-141430/14.

XX DR N-PSDB; ADO26591.

XX New mucosa-associated lymphoid tissue-lymphoma associated translocation

XX protein, useful in diagnosing and treating tumors.

XX Disclosure, SEQ ID NO 58, 88pp; English.

XX The present invention relates to a method for characterisation of
 CC chromosome translocation T (11;18) (q21;q21) and its association with
 CC malignancies such as mucosa-associated lymphoid tissue (MLT)-lymphomas.
 CC Also disclosed are: the polynucleotide and polypeptide sequences for
 CC human mucosa-associated lymphoid tissue (MLT)-lymphoma associated
 CC translocation (MLT), and a novel mechanism of primary cell transformation

CC by expression of a fusion protein comprising at least apoptosis inhibitor
 CC 2 (APl2) fused to another protein such as MLT. The MLT polynucleotide and
 CC polypeptide sequences, and the method of the invention are useful in
 CC diagnosing and treating tumours. The present sequence represents human
 CC APl2.

XX Sequence 442 AA;

SO Query Match 54.2%; Score 211; DB 8; Length 442;
 Best Local Similarity 57.4%; Pred. No. 7e-17;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTGFWIVS--VNKEQLARAGFYALGSDKVKCFHCGGLTDMKSEDPWEQHA 58
 DB 255 HAARFKTFPMWPSVLVNPQLASAGFYVGNSDVVCFCDDGGLRCWESGDDPWVQHA 314
 QY 59 WYPCCKYL 66
 DB 315 WFPRCXYL 322

RESULT 40

ABP72159 ID ABP72159 standard; protein; 557 AA.

AC ABP72159;

DT 22-APR-2003 (first entry)

XX Inhibitor of apoptosis protein CIAP2.

XX Inhibitor of apoptosis; CIAP2; apoptosis; cancer; leukaemia; lymphoma;
 KM neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX Unidentified.

XX WO200304606-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002NO-US021002.

XX 03-JUL-2001; 2001US-00898158.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

XX DR N-PSDB; AB258104.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

XX treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 17A; 124pp; English.

XX The present sequence is the protein sequence of inhibitor of apoptosis
 CC protein CIAP2. The invention provides a nucleic acid, such as an
 CC antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAPI, MIAPI2,
 CC MIAPI3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 557 AA;

Query Match 54.2%; Score 211; DB 6; Length 557;
 Best Local Similarity 57.4%; Pred. No. 9.2e-17;

	Matches	39;	Conservative	6;	Mismatches	21;	Indels	2;	Gaps	1;
Qy	1	YEARIFTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCQGGITDWPSEDPMEQJAK	58							
Db	255	HARFKTFEWMPSVTLVNPQLASAGFYVGNDDVDKCFCCDGGILRCWESGDDPMVOJAK	314							
Qy	59	WYPGCKYL	66							
Db	315	WPRCEYL	322							

Search completed: June 15, 2005, 17:35:45
Job time : 116 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:32:02 ; Search time 31 Seconds
(without alignments)
158,930 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389

Sequence: 1 YEARIPTFGTWIYSVNKEOL.....KPSHPDWEHAKWPGCKYL 66

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	66	2	US-08-511-485-25
2	389	100.0	66	4	US-09-201-936-25
3	389	100.0	66	4	US-09-011-356-25
4	389	100.0	66	4	US-09-201-932-25
5	389	100.0	236	3	US-09-239-867-4
6	389	100.0	236	4	US-10-024-433-4
7	389	100.0	497	2	US-08-511-485-4
8	389	100.0	497	3	US-09-212-971-4
9	389	100.0	497	3	US-08-800-929A-4
10	389	100.0	497	3	US-09-617-053A-4
11	389	100.0	497	4	US-08-657-759-2
12	389	100.0	497	4	US-09-201-936-4
13	389	100.0	497	4	US-09-011-356-4
14	389	100.0	497	4	US-09-672-717-219
15	389	100.0	497	4	US-09-201-932-4
16	389	100.0	497	4	US-09-949-016-6032
17	366	94.1	66	2	US-08-511-485-24
18	366	94.1	66	4	US-09-201-936-24
19	366	94.1	66	4	US-09-011-356-24
20	366	94.1	66	4	US-09-201-932-24
21	366	94.1	496	2	US-08-511-485-10
22	366	94.1	496	3	US-09-212-971-10
23	366	94.1	496	3	US-08-800-929A-10
24	366	94.1	496	3	US-09-617-053A-10
25	366	94.1	496	4	US-09-201-936-10
26	366	94.1	496	4	US-09-011-356-10
27	366	94.1	496	4	US-09-672-717-225

28	366	94.1	496	4	US-09-201-932-10	Sequence 10, Appl
29	347	89.2	236	3	US-09-121-979-4	Sequence 4, Appl
30	347	89.2	236	3	US-09-332-319-4	Sequence 4, Appl
31	347	89.2	236	4	US-09-239-867-2	Sequence 2, Appl
32	347	89.2	236	4	US-10-024-433-2	Sequence 2, Appl
33	295	75.8	53	4	US-08-657-759-19	Sequence 19, Appl
34	249	64.0	50	3	US-08-975-080-28	Sequence 28, Appl
35	249	64.0	50	3	US-08-975-080-32	Sequence 28, Appl
36	249	64.0	50	3	US-08-975-080-32	Sequence 28, Appl
37	249	64.0	50	4	US-10-138-618-28	Sequence 28, Appl
38	249	64.0	50	4	US-10-138-618-29	Sequence 29, Appl
39	249	64.0	50	4	US-10-138-618-32	Sequence 32, Appl
40	211	54.2	68	2	US-08-511-485-26	Sequence 26, Appl
41	211	54.2	68	4	US-09-201-936-26	Sequence 26, Appl
42	211	54.2	68	4	US-09-011-356-26	Sequence 26, Appl
43	211	54.2	68	4	US-09-201-932-26	Sequence 26, Appl
44	211	54.2	442	4	US-09-579-6928-58	Sequence 58, Appl
45	211	54.2	604	2	US-08-511-485-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-25
Sequence 25, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-25
Query Match 100.0%; Score 389; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YEARIPTFGTWIYSVNKEOLARAGFYALGEGDYKCFHCGGLTDWKPSSDPWEHAKWY 60
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Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4
US-09-201-932-25
; Sequence 25, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDVKYKCFHCGGLTDMKPSDPMEOHAKMY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 5
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 633412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
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; PRIOR FILING DATE: 1998-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-239-867-4

Query Match 100.0%; Score 389; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1,1e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 60
 Db 4 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 63

Qy 61 PGCKYL 66
 Db 64 PGCKYL 69

RESULT 6
 US-10-024-433-4
 ; Sequence 4, Application US/10024433
 ; Patent No. 6797473
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Korneluk et al.
 ; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
 ; FILE REFERENCE: 07891/018002
 ; CURRENT APPLICATION NUMBER: US/10/024,433
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/239,867
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-433-4

Query Match 100.0%; Score 389; DB 4; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1,1e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 60
 Db 4 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 63

Qy 61 PGCKYL 66
 Db 64 PGCKYL 69

RESULT 7
 US-08-511-485-4
 ; Sequence 4, Application US/08511485
 ; Patent No. 5919912
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander B.
 ; APPLICANT: Baird, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA

; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/511,485
 ; FILING DATE: 04-AUG-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 07540/002001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 497 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: both
 ; MOLECULE TYPE: protein
 US-08-511-485-4

Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 60
 Db 265 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKMY 324

Qy 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 8
 US-09-212-971-4
 ; Sequence 4, Application US/09212971B
 ; Patent No. 6107041
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander B.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009002
 ; CURRENT APPLICATION NUMBER: US/09/212,971B
 ; CURRENT FILING DATE: 1998-12-16
 ; EARLIER APPLICATION NUMBER: 60/017,354
 ; EARLIER FILING DATE: 1996-04-26
 ; EARLIER APPLICATION NUMBER: 60/030,590
 ; EARLIER FILING DATE: 1996-11-14
 ; EARLIER APPLICATION NUMBER: 08/800,929
 ; EARLIER FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-212-971-4

Query Match 100.0%; Score 389; DB 3; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
|||||
Db 265 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 324

QY 61 PGCKYL 66
|||||
Db 325 PGCKYL 330

RESULT 9
US-08-800-929A-4
Sequence 4, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-4

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
|||||
Db 265 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 324

QY 61 PGCKYL 66
|||||

Db 325 PGCKYL 330

RESULT 10
US-09-617-053A-4
Sequence 4, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-4

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
|||||
Db 265 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDWKPSDDPWEQHAKEY 324

QY 61 PGCKYL 66
|||||
Db 325 PGCKYL 330

RESULT 11
US-08-657-759-2
Sequence 2, Application US/08657759
Patent No. 6511828
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Duckett, Colin S.
TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,759
FILING DATE: 31-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-2

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 60
DB 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 12
US-09-201-936-4
Sequence 4, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Liatou, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 60
DB 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 13
US-09-011-356-4
Sequence 4, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Liatou, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
EARLIER FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-011-356-4

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 60
DB 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 14
US-09-672-717-219
Sequence 219, Application US/09672717
Patent No. 6673917
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Lacasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
FILE OF INVENTION: Thereof
FILE REFERENCE: 07891/025001
CURRENT APPLICATION NUMBER: US/09/672,717
EARLIER FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 219
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-672-717-219

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 60
DB 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSSEDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 15

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US-09-201-932-4
; Sequence 4, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-4

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 16
US-09-949-016-6032
; Sequence 6032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6032
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6032

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330
```

```
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 17
US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 591912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/08/511,485
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-511-485-24

Query Match      94.1%; Score 366; DB 2; Length 66;
Best Local Similarity 95.5%; Pred. No. 2.7e-11;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 60
Db      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 60
Qy      61 PGCKYL 66
Db      61 PGCKYL 66

RESULT 18
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
US-09-201-936-24

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSBDPWEQHAKEY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330
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```

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24
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Query Match          94.1% Score 366; DB 4; Length 66;
Best Local Similarity 95.5% Pred. No. 2.7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 YEARIFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
    |||||
Db 1 YEARIVFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
```

```
Qy 61 PGCKYL 66
    |||||
Db 61 PGCKYL 66
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RESULT 19

```
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24
```

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Query Match          94.1% Score 366; DB 4; Length 66;
Best Local Similarity 95.5% Pred. No. 2.7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 YEARIFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
    |||||
Db 1 YEARIVFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
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```
Qy 61 PGCKYL 66
    |||||
Db 61 PGCKYL 66
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RESULT 20

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US-09-201-932-24
; Sequence 24, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-24
```

```
Query Match          94.1% Score 366; DB 4; Length 66;
Best Local Similarity 95.5% Pred. No. 2.7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
    |||||
Db 1 YEARIVFGTWIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPMEQHAKMY 60
```

```
Qy 61 PGCKYL 66
    |||||
Db 61 PGCKYL 66
```

RESULT 21

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US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

QY	61	PGCKYL	66
Db	324	PGCKYL	329

```

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E

```

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617, 053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMEQHAKEY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMDQHAKEY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 25
US-09-201-936-10
Sequence 10, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMEQHAKEY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMDQHAKEY 323
QY 61 PGCKYL 66

DB 324 PGCKYL 329

RESULT 26
US-09-011-356-10
Sequence 10, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-011-356-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMEQHAKEY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMDQHAKEY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 27
US-09-672-717-225
Sequence 225, Application US/09672717
Patent No. 6673917
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Therapeutic
FILE REFERENCE: 07891/025001
CURRENT APPLICATION NUMBER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 225
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-672-717-225

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSBDPMEQHAKEY 60

Db 264 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 28
US-09-201-932-10

/ Sequence 10, Application US/09201932A
/ Patent No. 6689562

/ GENERAL INFORMATION:

/ APPLICANT: Korneluk, Robert G.

/ APPLICANT: Mackenzie, Alexander E.

/ APPLICANT: Baild, Stephen

/ APPLICANT: Liston, Peter

/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

/ FILE REFERENCE: 07891/003004

/ CURRENT APPLICATION NUMBER: US/09/201,932A

/ CURRENT FILING DATE: 1998-12-01

/ EARLIER APPLICATION NUMBER: 09/011,356

/ EARLIER FILING DATE: 1998-02-04

/ EARLIER APPLICATION NUMBER: PCT/IB96/01022

/ EARLIER FILING DATE: 1996-08-05

/ EARLIER APPLICATION NUMBER: 08/576,956

/ EARLIER FILING DATE: 1995-12-22

/ EARLIER APPLICATION NUMBER: 08/511,485

/ EARLIER FILING DATE: 1995-08-04

/ NUMBER OF SEQ ID NOS: 45

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 10

/ LENGTH: 496

/ TYPE: PRT

/ ORGANISM: Mus musculus

US-09-201-932-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 60
Db 264 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 29
US-09-121-979-4

/ Sequence 4, Application US/09121979

/ Patent No. 6159709

/ GENERAL INFORMATION:

/ APPLICANT: Korneluk, Robert G.

/ APPLICANT: Holcik, Martin

/ TITLE OF INVENTION: XIAP IRRS AND USES THEREOF

/ FILE REFERENCE: 07891/021001

/ CURRENT APPLICATION NUMBER: US/09/121,979

/ CURRENT FILING DATE: 1998-07-24

/ NUMBER OF SEQ ID NOS: 4

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 4

/ LENGTH: 236

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-09-121-979-4

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 60
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 63

QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 30
US-09-332-319-4

/ Sequence 4, Application US/09332319

/ Patent No. 6171821

/ GENERAL INFORMATION:

/ APPLICANT: Korneluk, Robert G.

/ APPLICANT: Holcik, Martin

/ APPLICANT: Liston, Peter

/ TITLE OF INVENTION: XIAP IRRS AND USES THEREOF

/ FILE REFERENCE: 07891/021002

/ CURRENT APPLICATION NUMBER: US/09/332,319

/ CURRENT FILING DATE: 1999-06-14

/ EARLIER APPLICATION NUMBER: 09/121,979

/ EARLIER FILING DATE: 1998-07-24

/ NUMBER OF SEQ ID NOS: 30

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 4

/ LENGTH: 236

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-09-332-319-4

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 60
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 63

QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 31
US-09-239-867-2

/ Sequence 2, Application US/09239867

/ Patent No. 6331412

/ GENERAL INFORMATION:

/ APPLICANT: Robert G. Korneluk et al.

/ TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING

/ FILE REFERENCE: 07891/018002

/ CURRENT APPLICATION NUMBER: US/09/239,867

/ CURRENT FILING DATE: 1999-01-29

/ PRIOR APPLICATION NUMBER: 60/073,001

/ PRIOR FILING DATE: 1998-01-29

/ NUMBER OF SEQ ID NOS: 10

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 2

/ LENGTH: 236

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-09-239-867-2

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 60
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKKY 63

QY 61 PGCKYL 66
 DB 64 PGCKYL 69

RESULT 32
 US-10-024-433-2
 ; Sequence 2, Application US/10024433
 ; Patent No. 6797473
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Korneluk et al.
 ; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
 ; FILE REFERENCE: 07891/018002
 ; CURRENT APPLICATION NUMBER: US/10/024,433
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/239,867
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-433-2

Query Match 89.2%; Score 347; DB 4; Length 236;
 Best Local Similarity 84.8%; Pred. No. 4,4e-38;
 Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTGWTIVSYNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAKVY 60
 DB 4 YEARIPTGWTIVSYNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAKVY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69

RESULT 33
 US-08-657-759-19
 ; Sequence 19, Application US/08657759
 ; Patent No. 6511828
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Craig B.
 ; APPLICANT: Duckett, Colin S.
 ; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
 ; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/657,759
 ; FILING DATE: 31-MAY-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: ARCD:220
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 53 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-657-759-19

Query Match 75.8%; Score 295; DB 4; Length 53;
 Best Local Similarity 100.0%; Pred. No. 5.9e-32;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EQARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAKVYPGCKYL 66
 DB 1 EQARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAKVYPGCKYL 49

RESULT 34
 US-08-975-080-28
 ; Sequence 28, Application US/08975080
 ; Patent No. 6245523
 ; GENERAL INFORMATION:
 ; APPLICANT: Altieri, Dario C.
 ; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 ; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 ; STREET: 1800 M Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036-5869
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,080
 ; FILING DATE: 20-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/031,435
 ; FILING DATE: 20-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adler, Reid G.
 ; REGISTRATION NUMBER: 30,988
 ; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-467-7176
 ; TELEFAX: 202-467-7176
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 50 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-975-080-28

Query Match 64.0%; Score 249; DB 3; Length 50;
 Best Local Similarity 100.0%; Pred. No. 7.2e-26;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCFHCGGLTDMKPSDPEQHAKVYPGCKYL 66
 DB 1 ALGEGDKVCFHCGGLTDMKPSDPEQHAKVYPGCKYL 40

RESULT 35
 US-08-975-080-29
 ; Sequence 29, Application US/08975080
 ; Patent No. 6245523

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-29

Query Match 64.0%; Score 249; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVRCFHGGGLTDWKPSDEPWEQAHAKYPGCKYL 66
Db 1 ALGEGDKVRCFHGGGLTDWKPSDEPWEQAHAKYPGCKYL 40

RESULT 36
US-08-975-080-32
Sequence 32, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-32

Query Match 64.0%; Score 249; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVRCFHGGGLTDWKPSDEPWEQAHAKYPGCKYL 66
Db 1 ALGEGDKVRCFHGGGLTDWKPSDEPWEQAHAKYPGCKYL 40

RESULT 37
US-10-138-618-28
Sequence 28, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 66
Db 1 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 40

RESULT 38

US-10-138-618-29

; Sequence 29; Application US/10138618

; Patent No. 6800737

; GENERAL INFORMATION:

; APPLICANT: Altieri, Dario C.

; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS

; CELLULAR APOPTOSIS, AND ITS MODULATION

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/138, 618

; FILING DATE: 06-May-2002

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/975, 080

; FILING DATE: 20-NOV-1997

; APPLICATION NUMBER: US 60/031,435

; FILING DATE: 20-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler, Reid G.

; REGISTRATION NUMBER: 30,988

; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-467-7000

; TELEFAX: 202-467-7176

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-138-618-29

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 66
Db 1 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 40

RESULT 39

US-10-138-618-32

; Sequence 32; Application US/10138618

; Patent No. 6800737

; GENERAL INFORMATION:

; APPLICANT: Altieri, Dario C.

; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS

; CELLULAR APOPTOSIS, AND ITS MODULATION

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/138, 618

; FILING DATE: 06-May-2002

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/975, 080

; FILING DATE: 20-NOV-1997

; APPLICATION NUMBER: US 60/031,435

; FILING DATE: 20-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler, Reid G.

; REGISTRATION NUMBER: 30,988

; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-467-7000

; TELEFAX: 202-467-7176

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-138-618-32

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 66
Db 1 ALGEGDVKKCFHCGGGLTDWKPSEDPEQHAQKYPGCKYL 40

RESULT 40

US-08-511-485-26

; Sequence 26; Application US/08511485

; Patent No. 5919912

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; AND DETECTION METHODS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/511,485

; FILING DATE: 04-AUG-1995

; CLASSIFICATION: 514

Thu Jun 16 13:06:37 2005

us-10-600-272-25.ra1

Page 14

```

? ATTORNEY/AGENT INFORMATION:
?
? NAME: Clark, Paul T.
? REGISTRATION NUMBER: 30,162
? REFERENCE/DOCKET NUMBER: 07540/002001
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: 617/542-5070
?
? TELEFAX: 617/542-8906
?
? TELER: 200154
?
? INFORMATION FOR SEQ ID NO: 26:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 68 amino acids
?
? TYPE: amino acid
?
? STRANDEDNESS: not relevant
?
? TOPOLOGY: both
?
? MOLECULE TYPE: protein
?
US-08-511-485-26

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Query Match	54.2%	Score 211	DB 20	Length 68
Best Local Similarity	57.4%	Pred. No.	1.2e-20	
Matches	39	Conservative	6	Mismatches 21
				Indels 2
				Gaps 1

Qy	1	YKARIFFFGFWIYS--VNKQLARAGFYALGSEDDKTCFCFCGGGLTDMKSPEDPMEQNAK	58
	:		:
	:		:
	:		:
	:		:
	:		:
Db	1	HAARFTFFFWPSSVLNPEQLASAGFYTGNSDDVCKFCDCDGLACWESGDDPFWQNAK	60
	:		:
	:		:
	:		:
	:		:
	:		:
Qy	59	WYPGCKTL	66
	:		:
	:		:
Db	61	WPPRCETL	68
	:		:
	:		:

Search completed: June 15, 2005, 17:53:09
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 15, 2005, 17:27:02 ; Search time 23.5 Seconds
(without alignments)
270.226 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIFFFTGWTIVSVNKEQL.....KPSEDPWEQHAQWPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	497	2	S69544 apoptotic inhibitor
2	211	54.2	604	2	S68449 apoptotic inhibitor
3	209	53.7	358	2	UC5964 apoptotic inhibitor
4	205	52.7	268	2	T10304 inhibitor of apopt
5	205	52.7	268	2	A53989 apoptotic-inhibiti
6	198	50.9	618	2	S68450 apoptotic inhibitor
7	190	48.8	275	2	A45679 inhibitor-of-apopt
8	188	48.3	298	2	JC7568 kidney inhibitor o
9	177.5	45.6	1232	2	A55478 neuronal apoptosis
10	174.5	44.9	1447	2	T42628 apoptotic inhibitor
11	162	41.6	496	2	S68452 apoptotic inhibitor
12	162	41.6	497	2	S69545 apoptotic inhibitor
13	144	37.0	208	2	T03183 probable apoptosi
14	139	35.7	150	2	T28409 ORF MSV248 probabl
15	125	32.1	275	2	T10310 apoptotic-inhibiti
16	115.5	29.7	4845	2	T31067 BIR repeat contain
17	111	28.5	286	2	D36828 orf13 protein - Au
18	109	28.0	292	2	T41772 IAP1 orf27 - Bomby
19	101	26.0	155	2	T30489 apoptotic inhibitor
20	100	25.7	155	2	T37471 apoptotic inhibitor
21	97	24.9	308	2	T37474 apoptotic inhibitor
22	87.5	22.5	329	2	T28403 ORF MSV242 probabl
23	87.5	22.5	997	2	T43523 A55R protein - fl
24	79.5	20.4	564	2	C42523 ORF MSV242 probabl
25	79.5	20.4	564	2	J01792 SaliF17R protein - vac
26	66	17.0	576	1	ACFP42 nicotinic acetylch
27	65	16.7	249	2	H72858 apoptosis inhibitor
28	65	16.7	444	2	T15907 hypothetical prote
29	65	16.7	1808	2	T15099 hypothetical prote

30	64.5	16.6	557	2	S12359 nicotinic acetylch
31	64.5	16.6	737	2	PQ0219 RNA-2 polypeptide
32	63.5	16.3	506	2	S13720 coat protein - ara
33	63.5	16.3	607	2	T39823 hypothetical prote
34	63	16.2	234	2	T30427 probable apoptosis
35	62.5	16.1	324	2	S39502 vegetative storage
36	62.5	16.1	532	2	A32751 speract receptor p
37	62	15.9	249	2	T41814 IAP2 orf71 - Bomby
38	62	15.9	474	2	S28419 lamin B2 - mouse
39	62	15.9	592	2	B48315 nicotinic acetylch
40	61	15.7	511	2	T43634 hypothetical prote
41	61	15.7	534	2	T25720 hyaluronate lyase
42	61	15.7	776	2	T29064 probable dna-3-met
43	60	15.4	204	2	H70609 MHC class II histo
44	60	15.4	246	2	T50127 MHC class II histo
45	60	15.4	252	2	I50126

ALIGNMENTS

```
RESULT 1
S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69544; S68451
R:Duckett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillefilian, M.C
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: UNIPROT:P98170; EMBL:U32974; NID:G1016687; PIDN:AAC50518.1; PID:G1016687
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahanf,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:G1184319; PIDN:AAC50373.1; PID:G1184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 YEARIFFFTGWTIVSVNKEQLAAGFYALGSGDKVCFHCGGGLTDMKPSEDPWEQHAQWY 60
Db 265 YEARIFFFTGWTIVSVNKEQLAAGFYALGSGDKVCFHCGGGLTDMKPSEDPWEQHAQWY 324

Cy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 2
S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahanf,
```

Nature 379, 343-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIIP and a related family of IAPs
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: UNIPROT:Q13489; EMBL:U45678; NID:g1184315; PIDN:PAC50371.1; PID:g118158
A:Function:
A:Description: apoptotic suppressor
A:Keywords: apoptosis; zinc finger
A:553-597/Domain: RING finger homology <RNG>

Query Match	54.2%	Score 211;	DB 2;	Length 604;
Best Local Similarity	57.4%	Pred. No. 2.9e-16;		
Matches 39;	Conservative 6;	Mismatches 21;	Indels 2;	Gaps 1;

[illegible]

RESULT 3
JC5964

apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: J05964
R:Steinhilb, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap) from
A:Reference number: J05964; MUID:98162622; PMID:9501011
A:Accession: J05964
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-358 (#STE>
A:Cross-references: UNIPROT:O62640; GB:U79142; NID:G2957174; PIDN:AA039177.1; PID:G2957174
A:307-351/Domain: RING finger homology <RNR>

Query Match	53.7%	Score 209;	DB 2;	Length 358;
Best Local Similarity	55.9%	Pred. No. 2.9e-16;		
Matches 38;	Conservative 7;	Mismatches 21;	Indels 2;	Gaps 11;

Qy 1 YEALIFPGGTIYS--VNKEOLAPAGFALBEGDVYKCEHGGGILTMDKRPSDPMPEHAK 58
 | : ||| ||||| : ||||| : ||| : |||
Db 90 YAAAFKTFICNPPSSLPVHPBOLASAGFYMGSHSDVKFCDDGGGLRCWESGDPPWEHAK 149
 | : ||| ||||| : ||||| : ||| : |||
Qy 59 WYPGCKYL 66
 | : ||| ||||| : ||||| : ||| : |||
b 150 WPRRCBYL 157

RESULT 4
T10304

Amino acid sequence of the Oryzias pseudotsugata nuclear polyhedrosis virus
C/SpecIES: Oryzias pseudotsugata nuclear polyhedrosis virus, OPMNV
C/Date: 16-Jul-1999 #sequence_revision 15-Jul-1999 #text_change 15-Sep-2000
C/Accession: F103031

R.Altrens, C.A.; Russell, R.R.; Funk, C.U.; Evans, J.; Rohrmann, G.F.
Virology 229, 381-399, 1997

A>Title: The sequence of the Oryzias pseudotsugata multi-nucleocapsid nuclear polyhedrosis virus
A/Reference number: Z17011; MUID:97273300; PMID:9126251

A:Accession: F10304
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-references: EMBL:U075930; NID:G2934903; PIDD:AA059034.1; PIDD:G1911281
C:Superfamily: Vital apoptosis inhibitor IAP; RING finger homology
C:217-261/Domain: RING finger homology <REN>

Query Match	52.7%	Score 205;	DB 2;	Length 268;
Best Local Similarity	50.0%;	Pred. No. 6.3e-16;		
Matches 33; Conservative	13;	Mismatches 18;	Indels 2;	Gaps 1;

```
QY      3  ARIFFGTWIVSVNK--EQLARAGFYALGEGDKVKCFPCGGGLTDWKPSBSPMECHAKWY 60
      ||: ||      : : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db     113 ARLRTFAEWPGILKQPEELLEAGFYATGGDITRCCFCDDGLKDWEPDPAWMOCHAWY 17
```

QY	61	PGCKYL	66
	:	:	
Db	173	DRCEYV	178

RESULT 5
A53989

Apoptosis-inhibiting protein - Orygia pseudotsugata nuclear polydrosis virus
 Apoptosis-inhibiting protein - Orygia pseudotsugata nuclear polydrosis virus
 C1species: Orygia pseudotsugata multicapsid nuclear polydrosis virus, OryNPV
 C1date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C1accession: A53989
 R:Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
 J. Virol. 68, 2521-2528, 1994
 A1title: An apoptosis-inhibiting gene from a nuclear polydrosis virus encoding a polypeptide
 A1reference number: A53989; NUID:34187094; PMID:8139034

A.Accession: A53989
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-268 <Bir>
A.Cross-references: UNIPROT:P41437; GB:J2564; NID:G45611; PID:G45614
A.Note: authors translated the codon TGG for residue 28 as 'Yr', GAC for residue 50 as Asr
C.Superfamily: viral apoptosis inhibitor IAP; RING finger homology
P.217-261/Domain: RING finger homology <RR>

Query Match	52.7%	Score 205;	DB 2;	Length 266;
Best Local Similarity	50.0%	Pred. No. 6.3e-16;		
Matches 33; Conservative	13;	Mismatches 18;	Indels 2;	Gaps 1;

```
OY      3 ARIPTGWTIYSVNK--EQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWEQHAKMY 60
        ||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      113 ARLRFAEWGRGLKQRPBEILAEGFYTGOGCKTRCCDDGLKDMEPDAPMOOHARMY 17
```

QY	61	PGCKYL	66
		:: :	
Db	173	DRCEYV	178

```

RESULT 6
S68450
apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_17-Jul-1998 #text_change 09-Jul-2004*
#accession: S68450

```

A:Title: Suppression of apoptosis in mammalian cells by NARP and a related family of IAP
 A:Reference number: A58182; MVID:96149249; PMID:8552191

A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-518 <LIS>
A:Cross-references: UNIPROT:O13490; EMBL:U45879; NID:g1184317; PIDD:AAC50372.1; PID:g1184317
C:Function:
A:Description: apoptotic suppressor
A:Keywords: apoptosis; zinc finger
A:567-611/Domain: RING finger homology <RNG>

Query Match	50.9%	Score 198;	DB 2;	Length 618;
Best Local Similarity	52.9%	Pred. No. 9.2e-15;		
Matches 36;	Conservative 9;	Mismatches 21;	Indels 2;	Gaps 1;

```

OY      1 YEARIFFTGTHWIS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDWKPSDDPWEQHAH 58
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
DB      269 HAARMRTFYMPSPVPVQPEQLASAGFYVYGRNDVVKCFGCDGGIRCMESGDDPWEZHAH 328

```

QY 59 WYPCCKYL 66
|:|:|:
Db 329 WPPKCEFL 336

RESULT 7

A45679
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C/Species: Cydia pomonella granulosis virus CpGV
C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: A45679
R/Crook, N.E.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A/Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A/Reference number: A45679; MUID:93188168; PMID:8445726
A/Accession: A45679
A/Status: preliminary
A/Molecule type: DNA
A/Keywords: 1-275 <CRO>
A/Cross-references: UNIPROT:P41436; GB:L05494; NID:G289583; PIDN:AAA43835.1; PID:G289584
A/Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P:127015)
C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 48.8%; Score 190; DB 2; Length 275;

Best Local Similarity 47.0%; Pred. No. 3,4e-14;

Matches 31; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

QY 3 ARIFFTGTV--IYSVKEQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDEPWEQHA 60

Db 110 ARVASFNNPRCMKQREPMADAGFYTGVDNTRCFYCDGLDMWEDVDVPMQHVWF 169

QY 61 PGCKYL 66
|:|:|:

Db 170 DRCAIV 175

RESULT 8

JC7568

kidney inhibitor of apoptosis protein - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JC7568

R/Lin, J.H.; Deng, G.; Huang, Q.; Morse, J.

Biochem. Biophys. Res. Commun. 279, 820-831, 2000

A/Title: KIAA, a novel member of the inhibitor of apoptosis protein family.

A/Reference number: JC7568; MUID: 21092523; PMID:11162435

A/Contents: Fetal kidney

A/Accession: JC7568

A/Molecule type: mRNA

A/Residues: 1-298 <LIN>

A/Cross-references: UNIPROT:Q96CA5

C/Comment: This protein, a new member of the inhibitor of apoptosis protein family, play

C/Genetics:

A/Gene: KIAA

A/Map position: 20q13.3

C/Keywords: apoptosis

Query Match 48.3%; Score 188; DB 2; Length 298;

Best Local Similarity 49.3%; Pred. No. 6,2e-14;

Matches 33; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 2 EARIFFTGTV--IYSVKEQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDEPWEQHA 59

Db 88 ELRLASFDYDPLTAIEVPELLAAAGFPHGTQDKVRCFCYGLQSWKRGDDPWTETAKW 147

QY 60 YPGCKYL 66
|:|:|:

Db 148 FPPSCFL 154

RESULT 9

A55478
neuronal apoptosis inhibitory protein - human

N/Alternate names: NAIP

C/Species: Homo sapiens (man)

C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001

C/Accession: A55478

R/Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yaraghi, Z.; Farahani, R.; Baird, S.

d, T.O.; de Jong, P.J.; Suh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.

Cell 80, 167-178, 1995

A/Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi

A/Reference number: A55478; MUID:55112344; PMID:7813013

A/Accession: A55478

A/Molecule type: mRNA

A/Residues: 1-1232 <ROY>

A/Cross-references: GB:U19251

C/Genetics:

A/Gene: GDB:SMA@; SMA

A/Cross-references: GDB:120378; OMIM:600354; OMIM:253300

A/Map position: 5q12.2-5q13

A/Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote

F/94-110/Domain: transmembrane #status predicted <TM1>

F/470-477/Region: nucleotide-binding motif A (P-loop)

F/479-496/Domain: transmembrane #status predicted <TM2>

F/476/Binding site: ATP (Lys) #status predicted

F/618,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 45.6%; Score 177.5; DB 2; Length 1232;

Best Local Similarity 42.6%; Pred. No. 4e-12;

Matches 29; Conservative 16; Mismatches 20; Indels 3; Gaps 1;

QY 2 EARIFFTGTV--IYSVKEQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDEPWEQHA 58

Db 160 EARLASFRNPFYVGISPCVLSBAGFVFTGKQDVTQCFSCGGLGMBEGDDPMKEHA 219

QY 59 WYPCCKYL 66
|:|:|:

Db 220 WPPKCEFL 227

RESULT 10

T42628

neuronal apoptosis inhibitory protein 2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T42628

R/Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.

Mamm. Genome 10, 761-763, 1999

A/Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murin

A/Reference number: Z22179; MUID:9315342; PMID:10384056

A/Accession: T42628

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1447 <YAR>

A/Cross-references: UNIPROT:Q9QUK4; EMBL:AF102871; NID:G3860228; PID:G3860229; PIDN:AACT7

C/Genetics:

A/Gene: Naip2

Query Match 44.9%; Score 174.5; DB 2; Length 1447;

Best Local Similarity 42.6%; Pred. No. 1e-11;

Matches 29; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

QY 2 EARIFFTGTV--IYSVKEQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDEPWEQHA 58

Db 160 EARLESDEMPFAHGRSPVLSAAGFVFTGKQDVTQCFSCGGLGMBEGDDPMKEHA 219

QY 59 WYPCCKYL 66
|:|:|:

Db 220 WPPKCEFL 227

RESULT 11

568452

apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)

F;223-268/Domain: RING finger homology <RRN>

Query Match 32.1%; Score 125; DB 2; Length 275;
Best Local Similarity 36.4%; Pred. No. 9e-07;
Matches 24; Conservative 11; Mismatches 29; Indels 2; Gaps 1;

QY 3 ARIFTFTWIVSN--KEQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPWEQHAQWY 60
DB 128 ARBATFPHMPPALNALTHDIAEAGMFTMLGDETFACFCDCRVRVMDLPQDDPQWQHALAN 187

QY 61 PGCKYL 66
DB 188 PGCFYFV 193

RESULT 16

BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31067

R;Hauser, H.P.; Bardroff, M.; Pyrowolskie, G.; Jentsch, S.

J. Cell Biol. 141, 1415-1422, 1998

A/Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.

A/Reference number: Z20963; MUID:98292517; PMID:9628897

A/Accession: T31067

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-4845 <HAU>

A/Cross-references: UNIPROT:O88738; EMBL:Y1267; NID:9331989; PIDN:CAA76720.1; PID:9331

A/Note: localized to the Golgi compartment and the vesicular system

C/Keywords: membrane-associated protein

Query Match 29.7%; Score 115.5; DB 2; Length 4845;
Best Local Similarity 31.3%; Pred. No. 0.00019;
Matches 21; Conservative 14; Mismatches 25; Indels 7; Gaps 2;

QY 7 TFGTFTS---VNKEQLARAGFY---ALGEGDKVYCFHCGGGLTDWKPSEDPWEQHAQW 59
DB 267 TFTSMPIVGRVWQAPDRMAQGFTHQPARSSGDDPMKCFTCVCLVCEPDEPMSHERH 326

QY 60 YPGCKYL 66
DB 327 SPNCPFV 333

RESULT 17

orf13 protein - Autographa californica nuclear polyhedrosis virus

C/Species: Autographa californica nuclear polyhedrosis virus, AcNPV
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: D36828; C72853
R;Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.

Virology 191, 1003-1008, 1992

A/Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica

VP8 of reovirus.

A/Reference number: A44221; MUID:93079853; PMID:1333113

A/Accession: D36828

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 <BRA>

A/Cross-references: UNIPROT:P41435; GB:S52569

R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A/Reference number: A72850; MUID:94303173; PMID:8030224

A/Accession: C72853

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-199, 'L', 201-286 <AYR>

A/Cross-references: GB:L22858; NID:9510708; PIDN:AAA6657.1; PID:9559096

C/Genetics: A;Gene: Ac-IAP1

C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 28.5%; Score 111; DB 2; Length 286;
Best Local Similarity 38.3%; Pred. No. 3.7e-05;
Matches 18; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 20 LABAGFYALGEGDKVYCFHCGGGLTDWKPSEDPWEQHAQWYPGCKYL 66
DB 153 IAEAGLFYTGGRGDETVCFDCDCVRDWMHTEDTQGHAAENPQCFYFV 199

RESULT 18

T41772

IAP1 orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C/Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV

A/Variety: isolate T3

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T41772

R;Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A/Reference number: Z22020; MUID:99281911; PMID:10355780

A/Accession: T41772

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-292 <KAM>

A/Cross-references: UNIPROT:Q92394; EMBL:L33180; NID:93745835; PIDN:AAC63701.1; PID:93745

A/Experimental source: isolate T3

C/Genetics: A;Note: IAP1

C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 28.0%; Score 109; DB 2; Length 292;
Best Local Similarity 38.3%; Pred. No. 6.5e-05;
Matches 18; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 20 LABAGFYALGEGDKVYCFHCGGGLTDWKPSEDPWEQHAQWYPGCKYL 66
DB 153 IAEAGLFYTGGRGDETVCFDCDCVRDWMHTEDTQGHAAENPQCFYFV 199

RESULT 19

apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus

C/Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30489
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 253, 17-34, 1999

A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d

A/Reference number: Z20836; MUID:99124785; PMID:9887315

A/Accession: T30489

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-155 <XUZ>

A/Cross-references: UNIPROT:Q9YMI9; EMBL:AF081810; PIDN:AAC70325.1

Query Match 26.0%; Score 101; DB 2; Length 155;
Best Local Similarity 29.2%; Pred. No. 0.00028;
Matches 19; Conservative 13; Mismatches 31; Indels 2; Gaps 1;

QY 4 RIPTFTW--IYVNKEQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPWEQHAQWY 61
DB 7 RLASFPMNSAVDPAAPAEIHAAGFYCANRDPFKCAVCHIEIENWISIGDAMSDBKRYSP 66

QY 62 GCKYL 66
DB 67 ACRFV 71

RESULT 20

T37471

apoptosis inhibitor homolog T37F2.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37471, T25380
R/Uren, A.G.
Submitted to the EMBL Data Library, January 1997
A:Description: C. elegans IAP homologue.
A:Reference number: Z21708
A/Accession: T37471
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-155 <URE>
A/Cross-references: UNIPROT:Q22837, EMBL:U85911, PIDD:AA894330.1
R/Iennard, N.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z20025
A/Accession: T25380
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-155 <WIL>
A/Cross-references: EMBL:Z74045, NID:e1062212, PIDD:CAA98553.1, GSPDB:GN00023, CESP:T27H
C/Genetics:
A/Map position: 5
A/Introns: 41/3

Query Match 25.7%; Score 100; DB 2; Length 155;
Best Local Similarity 31.9%; Pred. No. 0.00037;
Matches 23; Conservative 12; Mismatches 29; Indels 8; Gaps 3;

Qy 1 YEARIFPGWIVY-----SYNKEQLARAGFYALGEGDKYCFHGGGLTDMKSEDPWE 54
Db 17 YKDLMTFKNFEXRDPDAKCTSOAVAGFYCTGP-QSGKCAPCKNEL-DPDEDPMY 74

Qy 55 QHAKYPGCKYL 66
Db 75 EHTKRDSPCEYV 86

RESULT 21
T37474
apoptosis inhibitor homolog CS088.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37474, T20098
R/Uren, A.G.
Submitted to the EMBL Data Library, September 1996
A:Reference number: Z21711
A/Accession: T37474
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-308 <URE>
A/Cross-references: UNIPROT:Q18727, EMBL:U72208, PIDD:AA000182.1
R/Percy, C.
Submitted to the EMBL Data Library, July 1996
A:Reference number: Z19223
A/Accession: T20098
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-308 <WIL>
A/Cross-references: EMBL:Z77654, PIDD:CA801130.1, GSPDB:GN00023, CESP:CS088.2
C/Genetics:
A/Map position: 5
A/Introns: 48/3; 143/1; 191/3

Query Match 24.9%; Score 97; DB 2; Length 308;
Best Local Similarity 30.7%; Pred. No. 0.0016;
Matches 23; Conservative 20; Mismatches 22; Indels 10; Gaps 4;
Qy 1 YEARIFPGWIVYVKN-----EQLARAGFYAL-GSGDK-VKCFHGGGLTDMKSESD 51
Db 17 YKDLMTFKNFEXRDPDAKCTSOAVAGFYCTGP-QSGKCAPCKNEL-DPDEDPMY 74

Db 167 FDRHLPQNFIPDKRNVKTSKLUAKAGWBSIANKKDTSKACPCLVEL-DPDESD 225
Qy 52 PWEQHAKYPGCKYL 66
Db 226 PWEHQFASASCDPI 240

RESULT 22
T28403
ORF MSV242 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomox
C/Species: Melanoplus sanguinipes entomoxvirus
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T28403
R/Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomoxvirus.
A:Reference number: Z20484, NID:99102612, PMID:9847359
A/Accession: T28403
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-329 <AFO>
A/Cross-references: UNIPROT:Q9YVK0, EMBL:AF063866, NID:g4049647, PIDD:AAC97721.1, PIDD:g4(
C/Genetics:
A/Note: MSV242

Query Match 22.5%; Score 87.5; DB 2; Length 329;
Best Local Similarity 31.6%; Pred. No. 0.021;
Matches 18; Conservative 10; Mismatches 28; Indels 1; Gaps 1;

Qy 7 TRGCTWIVSVNKEQLARAGFYALGEGDKYCFHGGGLTDMKSEDPWEQHAKYPPG 63
Db 17 TYDKWNSLEIYVMWNAFTCKGP-SIVCEBCKRYLTWKKGDNPFEHIYYSKDC 72

RESULT 23
T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43523, T41649, T41700
R/Morioka, J.; Matsusaka, T.; Yanagida, M.
Submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cut17 is required for chromosome segregation.
A:Reference number: Z22536
A/Accession: T43523
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-997 <MOR>
A/Cross-references: UNIPROT:Q14064, EMBL:AB031034, PIDD:BA83415.1
R/Harris, D.; Wood, V.; Rajandream, M.A.; Barrett, B.G.
Submitted to the EMBL Data Library, August 1998
A:Reference number: Z22007
A/Accession: T41649
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-997 <HAR>
A/Cross-references: EMBL:AF031323, PIDD:CAA20434.1, GSPDB:GN00068, SPDB:SPCC962.02C
A/Experimental source: strxin 97ch-; cosmid c962
R/Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrett, B.G.
Submitted to the EMBL Data Library, October 1999
A:Reference number: Z22010
A/Accession: T41700
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 932-997 <MED>
A/Cross-references: EMBL:AL121859, PIDD:CA858376.1, GSPDB:GN00068, SPDB:SPCP31B10.10C
C/Genetics:
A/Map position: 3L
A/Introns: 43/3

Query Match 22.5%; Score 87.5; DB 2; Length 997;
Best Local Similarity 30.3%; Pred. No. 0.063;

Matches 23; Conservative 9; Mismatches 33; Indels 11; Gaps 3;
Qy 1 YEAFITFGTIVSYVNK---EQIARAGFY--ALGEG-----DKVCFHGGGLTDMKPS 49
Db 22 YSKRLDTQKKKMPRAKPTPETLATVGFYYPISHSNBEKLDNVTCTMCTKSPFDWEDD 81
Qy 50 EDPWEQHAQWYPCCKY 65
Db 82 DDLPEKHITHTSPSCPW 97
RESULT 24
C42523
A55R protein - vaccinia virus (strain Copenhagen)
C/Species: vaccinia virus
A/Note: host Homo sapiens (man)
C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C/Accession: C42523
R/Johnson, G.P.
submitted to GenBank, June 1990
A/Accession: C42523
A/Reference number: A33172
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <JOH>
A/Cross-references: UNIPROT:P21073
C/Superfamily: uncharacterized conserved protein with kelch repeats, vaccinia F3L type;
F/7-110/Domain: POZ domain homology <POZ>

Query Match 20.4%; Score 79.5; DB 2; Length 564;
Best Local Similarity 24.7%; Pred. No. 0.29;
Matches 19; Conservative 17; Mismatches 22; Indels 19; Gaps 4;
Qy 3 ARITFGT---WYSVNKEQLARAGFYALGEGDKVKCFHGGGLT-----WK 47
Db 313 SKVAIVTCTNSWYDIPELKYPRSNCGGLADDEYI---YCIIGIRDQSSLTSSIDKWK 369
Qy 48 PSEDPWEQHAQW-YPCG 63
Db 370 PSKRYWQKVAQMRPEKC 386

RESULT 25
JQ1792
SalF17R protein - vaccinia virus
N/Alternate names: SalF2R 64.7K protein
C/Species: vaccinia virus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JQ1792; C38550
R/Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A/Title: Nucleotide sequence of 428bp of vaccinia virus strain WR from near the right in
A/Reference number: JQ1767; MUID:91255063; PMID:2045793
A/Accession: JQ1792
A/Molecule type: DNA
A/Residues: 1-564 <SMI>
A/Cross-references: UNIPROT:P24768; DDBJ:D11079; NID:g222717; PIDN:BA01828.1; PID:g2227
A/Experimental source: strain WR
R/Howard, S.T.; Chan, Y.S.; Smith, G.L.
Virol. 180, 633-647, 1991
A/Title: Vaccinia virus homologues of the Shope fibroma virus inverted terminal repeat F
A/Reference number: A38550; MUID:91111982; PMID:1846491
A/Accession: C38550
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <HOW>
A/Cross-references: GB:M58052
A/Experimental source: strain WR
C/Superfamily: uncharacterized conserved protein with kelch repeats, vaccinia F3L type;
F/7-110/Domain: POZ domain homology <POZ>

Query Match 20.4%; Score 79.5; DB 2; Length 564;
Best Local Similarity 24.7%; Pred. No. 0.29;

Matches 19; Conservative 17; Mismatches 22; Indels 19; Gaps 4;
Qy 3 ARITFGT---WYSVNKEQLARAGFYALGEGDKVKCFHGGGLT-----WK 47
Db 313 SKVAIVTCTNSWYDIPELKYPRSNCGGLADDEYI---YCIIGIRDQSSLTSSIDKWK 369
Qy 48 PSEDPWEQHAQW-YPCG 63
Db 370 PSKRYWQKVAQMRPEKC 386

RESULT 26
ACFPA2
nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanog)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S11679; S10306; S11084
R/Sawruk, B.; Schloos, P.; Betz, H.; Schmitt, B.
EMBO J. 9, 2671-2677, 1990
A/Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel devel
A/Reference number: S11679; MUID:90360975; PMID:1697262
A/Accession: S11679
A/Molecule type: mRNA
A/Residues: 1-576 <SAW>
A/Cross-references: UNIPROT:P17644; EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A/Note: 233-ile was also found
R/Baumann, A.; Jonas, P.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 3640, 1990
A/Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acetyl
A/Reference number: S10306; MUID:90301489; PMID:2114015
A/Accession: S10306
A/Molecule type: mRNA
A/Residues: 1-576 <BAU>
A/Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803
R/Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, E.D.
FEBS Lett. 269, 264-268, 1990
A/Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel n
A/Reference number: S11084; MUID:90353591; PMID:2117557
A/Accession: S11084
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 42-90, '1', 92-576 <JON>
C/Genetics:
A/Gene: FLYBase:ACR-alpha-96b
A/Cross-references: FlyBase:FBgn0000039
A/Map position: 3R 96A
A/Intons: 84/3; 136/2; 196/3; 250/1; 445/2; 512/3
C/Superfamily: acetylcholine receptor
C/Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F/1-41/Domain: signal sequence #status predicted <SIG>
F/42-576/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
F/42-260/Domain: extracellular #status predicted <EXT>
F/261-287/Domain: transmembrane #status predicted <TM1>
F/293-311/Domain: transmembrane #status predicted <TM2>
F/327-348/Domain: transmembrane #status predicted <TM3>
F/349-326/Domain: intracellular #status predicted <INT>
F/557-545/Domain: transmembrane #status predicted <TM4>
F/65,254,570/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/169-183/Diulfide bonds: #status predicted

Query Match 17.0%; Score 66; DB 1; Length 576;
Best Local Similarity 29.0%; Pred. No. 11;
Matches 18; Conservative 10; Mismatches 24; Indels 10; Gaps 2;

Qy 8 FGTWYSVNKEQLARAGFYALGEGDKVKCFHGGGLTDMKPSD-----PWEQHAQWY 61
Db 187 FGSWTYDQGDIDLK---HISQKNDKDNKVEIGIDREYVPSVEMWILGVARHHEKYY 242
Qy 62 GC 63
Db 243 CC 244

RESULT 27
H72858
apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
C/Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A/Note: daDNA virus
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: H72858
R/Author: M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A/Reference number: A72850; MUID:94303173; PMID:8030224
A/Accession: H72858
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <AVR>
A/Cross-references: UNIPROT:P41454; GB:L22858; NID:G510708; PIDN:AAA6701.1; PID:G55914C
C/Genetics:
A/Genes: Ac-IAP2

Query Match 16.7%; Score 65; DB 2; Length 249;
Best Local Similarity 32.1%; Pred. No. 5.9;
Matches 17; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

Qy 14 SYNVEQLARAGFYALGEGDKKCFHCGGLTDMKPSDPMWQHAKWPGCKYL 66
Db 103 SVVVDMLRGRGFYFGAGHLRCSGC-HYVKYKSVDDAQRHKO--NCKFL 151

RESULT 28
T15907
hypothetical protein E04F6.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15907
R/Author: A.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid E04F6.
A/Reference number: Z18427
A/Accession: T15907
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-444 <PAU>
A/Cross-references: UNIPROT:Q10059; EMBL:U28943; NID:G861333; PID:G861337; PIDN:AAA68358
A/Experimental source: strain Bristol N2
C/Genetics:
A/Genes: CESP:E04F6.6
A/Intons: 41/1; 73/2; 127/2; 173/2; 256/3; 367/3
C/Superfamily: Caenorhabditis elegans hypothetical protein E04F6.6

Query Match 16.7%; Score 65; DB 2; Length 444;
Best Local Similarity 32.8%; Pred. No. 11;
Matches 22; Conservative 4; Mismatches 25; Indels 16; Gaps 4;

Qy 9 GTW-----TYSVNEQLARAGFYALGEGDKKCFHCGGLTDMKPSDPMWQH--AK 58
Db 284 GTMSVKGIPTYPPIWEE-----GAIAGRLMNVPPGSGGYSIHIGVRDYSQYQIGAN 338

Qy 59 WYPGCKY 65
Db 339 WYEG-KY 344

RESULT 29
T15099
hypothetical protein W03F8.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15099
R/Author: D.; Bradshaw, H.; Kepler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03F8.
A/Reference number: Z18293
A/Accession: T15099

A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1808 <JOH>
A/Cross-references: UNIPROT:O44565; EMBL:AF039041; NID:G2736380; PID:G2736388; PIDN:AA594
A/Experimental source: strain Bristol N2; clone W03F8
C/Genetics:
A/Genes: CESP:W03F8.5
A/Map position: 4
A/Intons: 99/2; 255/2; 365/2; 435/3; 565/2; 975/2; 1055/2; 1602/3; 1719/3; 1766/1
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
F/797-842/Domain: laminin-type EGF-like homology <LEG>

Query Match 16.7%; Score 65; DB 2; Length 1808;
Best Local Similarity 25.0%; Pred. No. 43;
Matches 11; Conservative 9; Mismatches 8; Indels 16; Gaps 2;

Qy 32 DKVCFPCGCGGLTDMKPSDPM-----EQAKKY 60
Db 74 EQTKCFYC-DSRTMKPQREPYRLSHRIENVTVTEWDDKRWNY 116

RESULT 30
S12359
nicotinic acetylcholine receptor alpha-1L chain precursor - desert locust
C/Species: Schistocerca gregaria (desert locust)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: S12359
R/Author: J.; Buckingham, S.D.; Shingal, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
EMBO J. 9, 4391-4398, 1990
A/Title: Sequence and functional expression of a single alpha subunit of an insect nicot
A/Reference number: S12359; MUID:91092263; PMID:1702381
A/Accession: S12359
A/Molecule type: mRNA
A/Residues: 1-557 <MAR>
A/Cross-references: UNIPROT:P23414; EMBL:X55439; NID:G10133; PIDN:CAA39081.1; PID:G10134
C/Superfamily: acetylcholine receptor
C/Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F/1-23/Domain: signal sequence #status predicted <SIG>
F/245-557/Product: nicotinic acetylcholine receptor alpha-1L chain #status predicted <MAT>
F/245-266/Domain: transmembrane #status predicted <TM1>
F/274-295/Domain: transmembrane #status predicted <TM2>
F/308-329/Domain: transmembrane #status predicted <TM3>
F/501-523/Domain: transmembrane #status predicted <TM4>
F/47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 64.5; DB 2; Length 557;
Best Local Similarity 24.7%; Pred. No. 15;
Matches 18; Conservative 9; Mismatches 13; Indels 33; Gaps 3;

Qy 8 FGTWYSVNEQLARAGFYALGEGDKKCFH-----CGGGLTDMKPSD----- 51
Db 169 FGSMTY-----DGDQIDLKHNQKYDKNKVKVIGDLREYSPSEVWDIIG 212

Qy 52 -PWEGHAKWPGC 63
Db 213 VPAERHEKTYPC 225

RESULT 31
P00219
RNA-2 polypeptide - arabis mosaic virus (fragment)
N/Contains: coat protein
C/Species: arabis mosaic virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: P00219; P00220
R/Bertoli, D.J.; Harris, R.D.; Edwards, M.L.; Cooper, J.I.; Hawes, W.S.
J. Gen. Virol. 72, 1801-1809, 1991
A/Title: Transgenic plants and insect cells expressing the coat protein of arabis mosaic
A/Reference number: P00219; MUID:91341466; PMID:1875193
A/Accession: P00219
A/Molecule type: genomic RNA
A/Residues: 1-737

A/Cross-references: UNIPROT:Q65028; GB:D10086; NID:G221017; PIDN:BA00982.1; PID:d100145C

A:Experimental source: strain 11lac
A:Accession: FQ0220
A:Molecule type: protein
A:Residues: 233-252 <BE2>
C:Genetics:
A:Map position: segment RNA-2
C:Keywords: polyprotein
F:233-737/Product: coat protein #status experimental <COA>

Query Match 16.6%; Score 64.5; DB 2; Length 737;
Best Local Similarity 32.3%; Pred. No. 20;
Matches 20; Conservative 7; Mismatches 20; Indels 15; Gaps 4;

Qy 12 IYSVVKQQLARAGFYALGEGDKVK-----CFHCGGGL-----TDWKPSDEPWEQHAKYYP 61
Db 447 VYNNFNTLLS-----YYLGIGGVKGVKVAHCSPCTGTGIVLRVYSEMGVNTNMNQLFK-YP 501
62 GC 63
502 GC 503

RESULT 32
coat protein - arabis mosaic virus (fragment)
C:Species: arabis mosaic virus
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C:Accession: S13720; S77995
R:Steinbrenner, H.; Himmeler, G.; Maltanovich, D.; Kattlinger, H.
Nucleic Acids Res. 18, 7182, 1990
A:Title: Nucleotide sequence of AMV-capsid protein-gene.
A:Reference number: S13720; MUID:91088343; PMID:2263501
A:Accession: S13720
A:Molecule type: genomic RNA
A:Residues: 1-506 <STR>
A:Cross-references: UNIPROT:P24819; EMBL:X55460
A:Accession: S77995
A:Molecule type: protein
A:Residues: 2-21 <HIM>
C:Keywords: polyprotein
F:2-506/Product: coat protein #status predicted <COA>

Query Match 16.3%; Score 63.5; DB 2; Length 506;
Best Local Similarity 32.3%; Pred. No. 18;
Matches 20; Conservative 7; Mismatches 20; Indels 15; Gaps 4;

Qy 12 IYSVVKQQLARAGFYALGEGDKVK-----CFHCGGGL-----TDWKPSDEPWEQHAKYYP 61
Db 216 VYNNFNTLLS-----YYLGIGGVKGVKVAHCSPCTGTGIVLRVYSEMGVNTNMNQLFK-YP 270
62 GC 63
271 GC 272

RESULT 33
hyposensitized protein SPBC19P5.05C SPBC25D12.01C - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39823; T39989
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrall, B.G.; Boche, G.; Pohl, T.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z21882
A:Accession: T39823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-607 <LVN>
A:Cross-references: UNIPROT:O60164; EMBL:AL022599; PIDN:CAA18653.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-; cosmid c25D12
R:Lyne, M.; Rajandream, M.A.; Barrall, B.G.; Whithead, S.; Chillingworth, T.; Churcher,
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21897

A:Accession: T39989
A:Molecule type: DNA
A:Residues: 1-454 <LY2>
A:Cross-references: EMBL:AL031158; PIDN:CAA20097.1; GSPDB:GN00067; SPDB:SPBC25D12.01C
A:Experimental source: strain 972h-; cosmid c25D12
C:Genetics:
A:Gene: SPBC19P5.05C; SPBC25D12.01C
A:Map position: 2
A:Introns: 8/1, 64/1

Query Match 16.3%; Score 63.5; DB 2; Length 607;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 14; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 1 YEARIPTFGTWIY-SVNKEQLARAGFYALG 29
Db 413 YEKRIYIQPWVYDSINKGILERTDLYACG 442

RESULT 34
T30427
probable apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30427
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-234 <KUZ>
A:Cross-references: UNIPROT:Q9YMP8; EMBL:AF081810; PIDN:AACT0265.1

Query Match 16.2%; Score 63; DB 2; Length 234;
Best Local Similarity 25.4%; Pred. No. 9.4;
Matches 16; Conservative 10; Mismatches 37; Indels 0; Gaps 0;

Qy 4 RIPTFGTWIY-SVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKYYPGC 63
Db 90 RAFAAGCGKYGSDANALAACGFFYNGRCREAGCSRCGMVVVXKLQRGDDLVIYIHGVSPRC 149
64 KYL 66
150 APV 152

RESULT 35
S39502
vegetative storage protein wind.5 - western balsam poplar x cottonwood (fragment)
C:Species: Populus trichocarpa x Populus deltoides (western balsam poplar x cottonwood)
C>Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S39502
R:David, J.M.; Egeltkrou, B.E.; Coleman, G.D.; Chen, T.H.H.; Haiszig, B.E.; Rlemenscheit
Plant Mol. Biol. 23, 135-143, 1993
A:Title: A family of wound-induced genes in Populus shares common features with genes enc
A:Reference number: S39502; MUID:94033285; PMID:8106009
A:Accession: S39502
A:Molecule type: mRNA
A:Residues: 1-324 <DAV>
A:Cross-references: UNIPROT:Q41097; EMBL:L20233; NID:G309838; PID:G309839

Query Match 16.1%; Score 62.5; DB 2; Length 324;
Best Local Similarity 39.6%; Pred. No. 15;
Matches 19; Conservative 2; Mismatches 20; Indels 7; Gaps 2;

Qy 8 FGTVISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKYYP 53
Db 158 FGEPNTVPVNGENLLASVDY-----DKYKLFKSHSPQDVWVWPFSTISW 200

RESULT 36

A32751
 spectact receptor precursor - sea urchin (Strongylocentrotus purpuratus)
 C/Species: Strongylocentrotus purpuratus (purple urchin)
 C/Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
 C/Accession: A32751; A31267
 R/Dangott, L.J.; Jordan, J.B.; Bellet, R.A.; Garbers, D.L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 2128-2132, 1989
 A/Title: Cloning of the mRNA for the protein that crosslinks to the egg peptide spectact.
 A/Reference number: A32751; MUID:89184581; PMID:2538832
 A/Accession: A32751
 A/Molecule type: mRNA
 A/Residues: 1-352; 'G', 354-532 <DA2>
 A/Cross-references: UNIPROT:P16264; GB:J04518
 A/Note: the authors translated the codon CAC for residue 353 as Gly
 C/Keywords: membrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-532/Product: spectact receptor #status predicted <MAT>
 F:40-144/Domain: scavenger receptor cysteine-rich domain homology <SRC1>
 F:150-257/Domain: scavenger receptor cysteine-rich domain homology <SRC2>
 F:261-366/Domain: scavenger receptor cysteine-rich domain homology <SRC3>
 F:379-485/Domain: scavenger receptor cysteine-rich domain homology <SRC4>

Query Match 16.1%; Score 62.5; DB 2; Length 532;
 Best Local Similarity 25.4%; Pred. No. 24;
 Matches 17; Conservative 12; Mismatches 17; Indels 21; Gaps 4;

QY 1 YEARIFTFGTWISVNKEQLARAGFYALGEGDKVK-CFHCGGGLTDWKPSDDPWEQHAKWY 59
 Db 98 FGAHVTF--WVYKGN-----CLGNETRLDDCYH-----RPGRPFLGNCAQW 137

QY 60 YPGCKYL 66
 Db 138 AAGVECL 144

RESULT 37
 T41814
 IAP2 orf71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
 C/Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
 A/Variety: isolate T3
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T41814
 R/Gomi, S.; Majima, K.; Maeda, S.
 J. Gen. Virol. 80, 1323-1337, 1999
 A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
 A/Reference number: 222020; MUID:99281911; PMID:10355780
 A/Accession: T41814
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-249 <KAM>
 A/Cross-references: UNIPROT:O92435; EMBL:L33180; PTDN:AAC63743.1
 A/Experimental source: isolate T3
 C/Genetics:
 A/Note: iap2

Query Match 15.9%; Score 62; DB 2; Length 249;
 Best Local Similarity 30.2%; Pred. No. 13;
 Matches 16; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

QY 14 SVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWYPGCKYL 66
 Db 103 SVVVDMLARKGFYFGAGHLRCGCG-HIVFKYKSVDDAQRHKO--NCKFV 151

RESULT 38
 S28419
 lamin B-3 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C/Accession: S28419
 R/Furukawa, K.; Hotta, Y.
 EMBO J. 12, 97-106, 1993

A/Title: cDNA cloning of a germ cell specific lamin B(3) from mouse spermatocytes and an
 A/Reference number: S28419; MUID:93154351; PMID:8094052
 A/Accession: S28419
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-474 <RUR>
 A/Cross-references: UNIPROT:P48680; EMBL:D13455; NID:9220471; PTDN:BAA02708.1; PID:92204;
 C/Superfamily: cytoskeletal keratin

Query Match 15.9%; Score 62; DB 2; Length 474;
 Best Local Similarity 35.1%; Pred. No. 25;
 Matches 13; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 26 YALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWYPG 62
 Db 375 YVLRAGQTVVMAAGAGATHSPSTLWKSQTWVG 411

RESULT 39
 B48315
 lamin B2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: B48315; S08264; A41068; A56583; S21609
 R/Hoeger, T.H.; Zatloukal, K.; Walzenegger, I.; Krohne, G.
 Chromosoma 99, 379-390, 1990
 A/Title: Characterization of a second highly conserved B-type lamin present in cells pre
 A/Reference number: A48315; MUID:91106216; PMID:2102682
 A/Accession: B48315
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-592 <HOB>
 A/Cross-references: UNIPROT:P21619; EMBL:X54098; NID:952866; PTDN:CMA38032.1; PID:952867
 A/Note: the figure legends for Fig. 5 (African clawed frog) and Fig. 6 (mouse) appear to
 sequences in Genbank
 R/Hoeger, T.H.; Zatloukal, K.; Walzenegger, I.; Krohne, G.
 Chromosoma 100, 67-69, 1990
 A/Reference number: A56583; MUID:91339548; PMID:2102440
 A/Contents: annotation; extratum
 A/Note: corrects transposition of Figs. 5 and 6
 R/Weber, K.; Pleesmann, U.; Traub, P.
 FEBS Lett. 261, 361-364, 1990
 A/Title: Protein chemical analysis of purified murine lamin B identifies two distinct po
 A/Reference number: S08264; MUID:90184461; PMID:2311764
 A/Accession: S08264
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 182-206;234-286;290-313; 'R', 315-317; 'X', 319;364-401;466-479; 'X', 481-492 <WEB>
 R/Kasahara, K.; Chida, K.; Tsunenaga, M.; Kohno, Y.; Ikuta, T.; Kuroki, T.
 J. Biol. Chem. 266, 20018-20023, 1991
 A/Title: Identification of lamin B-2 as a substrate of protein kinase C in BALB/MK-2 mou
 A/Reference number: A41068; MUID:92041823; PMID:1939065
 A/Accession: A41068
 A/Molecule type: protein
 A/Residues: 165-166; 'X', 169; 'X', 170-172;254-258; 'X', 260-262;478-479; 'X', 481-483; 'X', 485-4
 C/Superfamily: cytoskeletal keratin
 C/Keywords: nucleus

Query Match 15.9%; Score 62; DB 2; Length 592;
 Best Local Similarity 35.1%; Pred. No. 31;
 Matches 13; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 26 YALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWYPG 62
 Db 493 YVLRAGQTVVMAAGAGATHSPSTLWKSQTWVG 529

RESULT 40
 T43634
 nicotinic acetylcholine receptor alpha chain - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43634

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OM protein - protein search, using SW model

Run on: June 15, 2005, 17:39:48 ; Search time 108.5 Seconds
(without alignments)
233.180 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIPTFGTWIYSVNKEQL.....KPSIEDPWCHAKMYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 38333425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pcp:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pcp:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pcp:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pcp:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pcp:*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pcp:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pcp:*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pcp:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pcp:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pcp:*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pcp:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pcp:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pcp:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pcp:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pcp:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pcp:*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pcp:*
- 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pcp:*
- 19: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pcp:*
- 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pcp:*
- 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pcp:*
- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	389	100.0	66 9 US-09-201-936-25	Sequence 25, Appl
2	389	100.0	66 16 US-10-600-272-25	Sequence 25, Appl
3	389	100.0	107 9 US-09-965-967-20	Sequence 20, Appl
4	389	100.0	236 13 US-10-024-433-4	Sequence 4, Appl
5	389	100.0	278 9 US-09-964-859-39	Sequence 39, Appl
6	389	100.0	497 9 US-09-974-592-4	Sequence 4, Appl
7	389	100.0	497 9 US-09-201-936-4	Sequence 4, Appl
8	389	100.0	497 15 US-10-366-307-2	Sequence 2, Appl
9	389	100.0	497 16 US-10-636-065-219	Sequence 219, Appl
10	389	100.0	497 16 US-10-600-272-4	Sequence 4, Appl
11	366	94.1	66 9 US-09-201-936-24	Sequence 24, Appl

12	366	94.1	66 16 US-10-600-272-24	Sequence 24, Appl
13	366	94.1	496 9 US-09-974-592-10	Sequence 10, Appl
14	366	94.1	496 9 US-09-201-936-10	Sequence 10, Appl
15	366	94.1	496 16 US-10-636-065-225	Sequence 225, Appl
16	366	94.1	496 16 US-10-600-272-10	Sequence 10, Appl
17	352	90.5	496 16 US-10-482-952-5	Sequence 5, Appl
18	347	89.2	236 13 US-10-024-433-2	Sequence 2, Appl
19	347	89.2	464 15 US-10-343-115-2	Sequence 2, Appl
20	249	64.0	50 14 US-10-138-618-28	Sequence 28, Appl
21	249	64.0	50 14 US-10-138-618-29	Sequence 29, Appl
22	249	64.0	50 14 US-10-138-618-32	Sequence 32, Appl
23	211	54.2	68 9 US-09-201-936-26	Sequence 26, Appl
24	211	54.2	68 16 US-10-600-272-26	Sequence 26, Appl
25	211	54.2	557 16 US-10-482-952-9	Sequence 9, Appl
26	211	54.2	604 9 US-09-974-592-6	Sequence 6, Appl
27	211	54.2	604 14 US-10-232-286-4	Sequence 6, Appl
28	211	54.2	604 14 US-10-141-618-6	Sequence 6, Appl
29	211	54.2	604 15 US-10-366-307-6	Sequence 6, Appl
30	211	54.2	604 15 US-10-636-065-221	Sequence 221, Appl
31	211	54.2	604 16 US-10-600-272-6	Sequence 6, Appl
32	211	54.2	604 16 US-10-730-476A-79	Sequence 79, Appl
33	211	54.2	604 16 US-10-825-282-40	Sequence 40, Appl
34	211	54.2	604 17 US-10-934-717-4	Sequence 4, Appl
35	211	54.2	1140 14 US-10-353-461-8	Sequence 8, Appl
36	205	52.7	68 9 US-09-201-936-28	Sequence 28, Appl
37	205	52.7	68 14 US-10-041-859-18	Sequence 18, Appl
38	205	52.7	68 16 US-10-600-272-28	Sequence 28, Appl
39	205	52.7	172 14 US-10-041-859-12	Sequence 12, Appl
40	205	52.7	268 14 US-10-323-643-10	Sequence 10, Appl
41	205	52.7	268 14 US-09-974-592-12	Sequence 12, Appl
42	203	52.2	600 9 US-10-482-952-1	Sequence 1, Appl
43	199	51.2	68 14 US-10-041-859-14	Sequence 14, Appl
44	199	51.2	172 14 US-10-041-859-8	Sequence 8, Appl
45	199	51.2		

ALIGNMENTS

RESULT 1
US-09-201-936-25
Sequence 25, Application US/09201936
Publication No. US20020167946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-10-600-272-25
; Sequence 25, Application US/10600272
; Publication No. US2004015732A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/1B96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-25

Query Match 100.0%; Score 389; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US2002017757A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

Query Match 100.0%; Score 389; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.2e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 15 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 74
Qy 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 4
US-10-024-433-4
; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-4

Query Match 100.0%; Score 389; DB 13; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 4 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 63
Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 5
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

Query Match 100.0%; Score 389; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;


```
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 60
Db 46 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 105
QY 61 PGCKYL 66
Db 106 PGCKYL 111

RESULT 6
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: MALE FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 60
Db 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 7
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
```

```
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 60
Db 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 8
US-10-366-307-2
; Sequence 2, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-307-2

Query Match 100.0%; Score 389; DB 15; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 60
Db 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMEOHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 9
US-10-636-065-219
; Sequence 219, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
```

;; PRIOR FILING DATE: 2000-09-28
;; NUMBER OF SEQ ID NOS: 231
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 219
;; LENGTH: 497
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-636-065-219

Query Match
Best Local Similarity 100.0%; Score 389; DB 16; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60
|||
Db 265 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 324

Qy 61 PGCKYL 66
|||
Db 325 PGCKYL 330

RESULT 10
US-10-600-272-4
; Sequence 4, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-4

Query Match
Best Local Similarity 100.0%; Score 389; DB 16; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60
|||
Db 265 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 324

Qy 61 PGCKYL 66
|||
Db 325 PGCKYL 330

RESULT 11
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

;; APPLICANT: Liston, Peter
;; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;; FILE REFERENCE: 07891/003003
;; CURRENT APPLICATION NUMBER: US/09/201,936
;; PRIOR FILING DATE: 1998-12-01
;; PRIOR APPLICATION NUMBER: 09/011,356
;; PRIOR FILING DATE: 1998-02-04
;; PRIOR APPLICATION NUMBER: PCT/IB96/01022
;; PRIOR FILING DATE: 1996-08-05
;; PRIOR APPLICATION NUMBER: 08/576,956
;; PRIOR FILING DATE: 1995-12-22
;; PRIOR APPLICATION NUMBER: 08/511,485
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match
Best Local Similarity 94.1%; Score 366; DB 9; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60
|||
Db 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60

Qy 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 12
US-10-600-272-24
; Sequence 24, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-600-272-24

Query Match
Best Local Similarity 94.1%; Score 366; DB 16; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60
|||
Db 1 YEARITFTGTWISVNVKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAKEY 60

OY 61 PGCKYL 66
 Db 61 PGCKYL 66

RESULT 13

US-09-974-592-10
 ; Sequence 10, Application US/09974592
 ; Patent No. US20020120121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Teang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009004
 ; CURRENT APPLICATION NUMBER: US/09/974,592
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: US 09/617,053
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/800,929
 ; PRIOR FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-974-592-10

Query Match 94.1%; Score 366; DB 9; Length 496;
 Best Local Similarity 95.5%; Pred. No. 1,6e-35;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEARIFPGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEOHAKWY 60
 Db 264 YEARIVTFGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKCY 323

OY 61 PGCKYL 66
 Db 324 PGCKYL 329

RESULT 14

US-09-201-936-10
 ; Sequence 10, Application US/09201936
 ; Publication No. US20020187946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; PRIOR FILING DATE: 1998-12-01
 ; PRIOR APPLICATION NUMBER: 09/011,356
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 496

TYPE: PRT
 ORGANISM: Mus musculus
 US-09-201-936-10

Query Match 94.1%; Score 366; DB 9; Length 496;
 Best Local Similarity 95.5%; Pred. No. 1,6e-35;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEARIFPGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEOHAKWY 60
 Db 264 YEARIVTFGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKCY 323

OY 61 PGCKYL 66
 Db 324 PGCKYL 329

RESULT 15

US-10-636-065-225
 ; Sequence 225, Application US/10636065
 ; Publication No. US20040127694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: LaCasse, Eric
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Holcik, Martin
 ; APPLICANT: Young, Sean
 ; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
 ; TITLE OF INVENTION: Theroot
 ; FILE REFERENCE: 07891/025005
 ; CURRENT APPLICATION NUMBER: US/10/636,065
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: 09/672,717
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 225
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-636-065-225

Query Match 94.1%; Score 366; DB 16; Length 496;
 Best Local Similarity 95.5%; Pred. No. 1,6e-35;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEARIFPGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEOHAKWY 60
 Db 264 YEARIVTFGTWISVKNKQIARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMDOHAKCY 323

OY 61 PGCKYL 66
 Db 324 PGCKYL 329

RESULT 16

US-10-600-272-10
 ; Sequence 10, Application US/10600272
 ; Publication No. US20040157232A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003006
 ; CURRENT APPLICATION NUMBER: US/10/600,272
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/011,356
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: PCT/IB96/01022
 ; PRIOR FILING DATE: 1996-08-05

```

; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-600-272-10

Query Match
Best Local Similarity 94.1%; Score 366; DB 16; Length 496;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 60
DB 264 YEARIVTFGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 17
US-10-482-952-5
; Sequence 5, Application US/10482952
; Publication No. US20040254136A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York, et al.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CEL
; FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
; CURRENT APPLICATION NUMBER: US/10/482,952
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 496
; TYPE: PRT
; ORGANISM: human
US-10-482-952-5

Query Match
Best Local Similarity 90.5%; Score 352; DB 16; Length 496;
Matches 61; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 60
DB 264 YEARIVTFGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 18
US-10-024-433-2
; Sequence 2, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneljuk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US/09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-2

Query Match
Best Local Similarity 89.2%; Score 347; DB 13; Length 236;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 60
DB 4 YEARLITFGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 19
US-10-343-115-2
; Sequence 2, Application US/10343115
; Publication No. US20040072999A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: Novel inhibitor of apoptosis protein
; FILE REFERENCE: IAPL-7BHM5
; CURRENT APPLICATION NUMBER: US/10/343,115
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-115-2

Query Match
Best Local Similarity 89.2%; Score 347; DB 15; Length 464;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 60
DB 232 YEARLITFGTWISVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPMWEOHAKMY 291
QY 61 PGCKYL 66
DB 292 PGCKYL 297

RESULT 20
US-10-138-618-28
; Sequence 28, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
```

SEQUENCE DESCRIPTION: SEQ ID NO: 29;
US-10-138-618-29

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 66
1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 40

RESULT 21
US-10-138-618-29
; Sequence 29, Application US/10138618
; Publication No. US20030100525A1

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 29;
US-10-138-618-29

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 66
1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 40

RESULT 22
US-10-138-618-32
; Sequence 32, Application US/10138618
; Publication No. US20030100525A1

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32;
US-10-138-618-32

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 66
1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKYPPGCKYL 40

RESULT 23
US-09-201-936-26
; Sequence 26, Application US/09201936
; Publication No. US20020187946A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26
```

```
Query Match          54.2%; Score 211; DB 9; Length 68;
Best Local Similarity 57.4%; Pred. No. 1,1e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
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```
QY 1 YEARIFPGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPWBOHAK 58
Db 1 HAARFKTFEWPBSSVLVNPBQLASAGFYVGNSDVACFCDDGLRCWBSGDDPWVOHAK 60
```

```
QY 59 WYPGCKYL 66
Db 61 WPPRCCEYL 68
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```

RESULT 24
US-10-600-272-26
; Sequence 26, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-26
```

```
Query Match          54.2%; Score 211; DB 16; Length 68;
Best Local Similarity 57.4%; Pred. No. 1,1e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
```

```

Db 1 HAARFKTFEWPBSSVLVNPBQLASAGFYVGNSDVACFCDDGLRCWBSGDDPWVOHAK 60
QY 59 WYPGCKYL 66
Db 61 WPPRCCEYL 68
```

```

RESULT 25
US-10-482-952-9
; Sequence 9, Application US/10482952
; Publication No. US20040254136A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York, et al.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CELL
; FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
; CURRENT APPLICATION NUMBER: US/10/482,952
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 9
; LENGTH: 557
; TYPE: PRT
; ORGANISM: human
US-10-482-952-9
```

```
Query Match          54.2%; Score 211; DB 16; Length 557;
Best Local Similarity 57.4%; Pred. No. 9,8e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
```

```
QY 1 YEARIFPGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPWBOHAK 58
Db 255 HAARFKTFEWPBSSVLVNPBQLASAGFYVGNSDVACFCDDGLRCWBSGDDPWVOHAK 314
```

```
QY 59 WYPGCKYL 66
Db 315 WPPRCCEYL 322
```

```

RESULT 26
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin X
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6
```

```
Query Match          54.2%; Score 211; DB 9; Length 604;
Best Local Similarity 57.4%; Pred. No. 1,1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
```

```

Db      255 HAARKTEFFNPSSVLVNPEQLASAGFYVGNSSDDVKCFCCGGGLRCWESGDDPWNQHAH 314
OY      59 WYPGCKYL 66
        ||:|:|
Db      315 WFPRCXYL 322

RESULT 27
US-09-201-936-6
/ Sequence 6, Application US/09201936
/ Publication No. US20020187946A1
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Mackenzie, Alexander E.
/ APPLICANT: Baird, Stephen
/ APPLICANT: Liston, Peter
/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
/ TITLE OF INVENTION: PROBES, AND DETECTION METHODS
/ FILE REFERENCE: 07891/003003
/ CURRENT APPLICATION NUMBER: US/09/201,936
/ CURRENT FILING DATE: 1998-12-01
/ EARLIER APPLICATION NUMBER: 09/011,356
/ EARLIER FILING DATE: 1998-02-04
/ EARLIER APPLICATION NUMBER: PCT/IB96/01022
/ EARLIER FILING DATE: 1996-08-05
/ EARLIER APPLICATION NUMBER: 08/516,956
/ EARLIER FILING DATE: 1995-12-22
/ EARLIER APPLICATION NUMBER: 08/511,485
/ EARLIER FILING DATE: 1995-08-04
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 604
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-201-936-6

Query Match      54.2%; Score 211; DB 9; Length 604;
Best Local Similarity 57.4%; Pred. No. 1,1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1.

OY      1 YEAR1FTGTGTYWS--VNKEQLARAGFYALGEGDKYKCHCGGGLTDWKSSDDPWNQHAH 58
Db      255 HAARKTEFFNPSSVLVNPEQLASAGFYVGNSSDDVKCFCCGGGLRCWESGDDPWNQHAH 314
OY      59 WYPGCKYL 66
        ||:|:|
Db      315 WFPRCXYL 322

RESULT 28
US-10-233-286-4
/ Sequence 4, Application US/10232286
/ Publication No. US20030143579A1
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Mike
/ APPLICANT: Goeddel, David V
/ TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: FLHER, HOHBACH, TEST, ALBRITTON & HERBERT
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ APPLICATION DATA:
/ APPLICATION NUMBER: US/10/232,286

```

```

/ / FILING DATE: 30-Aug-2002
/ / CLASSIFICATION: <Unknown>
/ / PRIOR APPLICATION DATA:
/ / APPLICATION NUMBER: US/08/569,749
/ / FILING DATE: <Unknown>
/ / ATTORNEY/AGENT INFORMATION:
/ / NAME: Brezner, David J.
/ / REGISTRATION NUMBER: 24,774
/ / REFERENCE/DOCKET NUMBER: A-62464/DJB
/ / TELECOMMUNICATION INFORMATION:
/ / TELEPHONE: (415)781-1989
/ / TELEFAX: (415)398-3249
/ / INFORMATION FOR SEQ ID NO: 4:
/ / SEQUENCE CHARACTERISTICS:
/ / LENGTH: 604 amino acids
/ / TYPE: amino acid
/ / STRANDEDNESS: single
/ / TOPOLOGY: linear
/ / MOLECULE TYPE: protein
/ / SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-232-286-4

Query Match 54.2% Score 211; DB 14; Length 604;
Best Local Similarity 57.4%; Pred. No. 1.1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARNFTFGWTIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAH 58
DB 255 HAARFKTFEFPNPSVVLVNPBQLASAGFYVGNSDVKCFCCDGGLRCHESGDDPWOVQAH 314
QY 59 WYPGCKYL 66
DB 315 WFPRCGYL 322

RESULT 29
US-10-141-618-6
/ / Sequence 6, Application US/10141618
/ / Publication No. US20030165887A1
/ / GENERAL INFORMATION:
/ / APPLICANT: Reed, John C.
/ / TITLE OF INVENTION: Methods For Determining the Prognosis
/ / TITLE OF INVENTION: For Cancer Patients Using Tucan
/ / FILE REFERENCE: P-LJ 5254
/ / CURRENT APPLICATION NUMBER: US/10/141.618
/ / CURRENT FILING DATE: 2002-05-07
/ / PRIOR APPLICATION NUMBER: US 60/289,233
/ / PRIOR FILING DATE: 2001-05-07
/ / PRIOR APPLICATION NUMBER: US 60/356,934
/ / PRIOR FILING DATE: 2002-02-12
/ / PRIOR APPLICATION NUMBER: US 09/388,221
/ / PRIOR FILING DATE: 1999-09-01
/ / NUMBER OF SEQ ID NOS: 15
/ / SOFTWARE: FastSeq for Windows Version 4.0
/ / SEQ ID NO 6
/ / LENGTH: 604
/ / TYPE: PRT
/ / ORGANISM: Homo sapiens
US-10-141-618-6

Query Match 54.2% Score 211; DB 14; Length 604;
Best Local Similarity 57.4%; Pred. No. 1.1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARNFTFGWTIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAH 58
DB 255 HAARFKTFEFPNPSVVLVNPBQLASAGFYVGNSDVKCFCCDGGLRCHESGDDPWOVQAH 314
QY 59 WYPGCKYL 66
DB 315 WFPRCGYL 322

```



```

RESULT 34
US-10-825-282-40
; Sequence 40, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; PRIORITY FILING DATE: 2004-04-14
; PRIORITY APPLICATION NUMBER: US/09/456,357
; PRIORITY FILING DATE: 1999-12-08
; PRIORITY APPLICATION NUMBER: 60/134,416
; PRIORITY FILING DATE: 1999-05-17
; PRIORITY APPLICATION NUMBER: 09/087,195
; PRIORITY FILING DATE: 1998-05-29
; PRIORITY APPLICATION NUMBER: 08/378,507
; PRIORITY FILING DATE: 1995-01-26
; PRIORITY APPLICATION NUMBER: 08/250,478
; PRIORITY FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-40

```

```

Query Match 54.2%; Score 211; DB 16; Length 604;
Best Local Similarity 57.4%; Pred. No. 1,1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARITFGTWIYS--VNKEQLAAGFYALGEGDKYKCFHCGGLTDMKPSDEDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322

```

```

RESULT 35
US-10-934-717-4
; Sequence 4, Application US/10934717
; Publication No. US20050037416A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/934,717
; FILING DATE: 03-Sep-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/332,286
; FILING DATE: 30-Aug-2002
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-934-717-4

```

```

Query Match 54.2%; Score 211; DB 17; Length 604;
Best Local Similarity 57.4%; Pred. No. 1,1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARITFGTWIYS--VNKEQLAAGFYALGEGDKYKCFHCGGLTDMKPSDEDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322

```

```

RESULT 36
US-10-353-461-8
; Sequence 8, Application US/10353461
; Publication No. US20030176682A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Internuiversteitair Instituut voor Biotechnol
; TITLE OF INVENTION: Molecular characterisation of chromosome translocation
; TITLE OF INVENTION: c(11;18) (q21;q21) and its correlation to
; FILE REFERENCE: PMA/MALT/V043
; CURRENT APPLICATION NUMBER: US/10/353,461
; CURRENT FILING DATE: 2003-01-26
; PRIORITY APPLICATION NUMBER: US/09/579,692
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: 60/138,834
; PRIORITY FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-461-8

```

```

Query Match 54.2%; Score 211; DB 14; Length 1140;
Best Local Similarity 57.4%; Pred. No. 2,1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARITFGTWIYS--VNKEQLAAGFYALGEGDKYKCFHCGGLTDMKPSDEDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322

```

```

RESULT 37
US-09-201-936-28
; Sequence 28, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Kornelink, Robert G.

```

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-09-201-936-28

```

```

Query Match          52.7%; Score 205; DB 9; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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Qy 3 ARITFGTWIYSVVK--EQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMEQHAKMY 60
Db 3 ARITFAMWRGRGLKQRPBELAENGFFYTGQDVKTRCCDGGGLKDWEPDAPWQHAKMY 62

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Qy 61 PGCKYL 66
Db 63 DRCEYV 68

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```

RESULT 38
US-10-041-859-18
; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-041-859-18

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Query Match          52.7%; Score 205; DB 14; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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Qy 3 ARITFGTWIYSVVK--EQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMEQHAKMY 60
Db 3 ARITFAMWRGRGLKQRPBELAENGFFYTGQDVKTRCCDGGGLKDWEPDAPWQHAKMY 62
Qy 61 PGCKYL 66
Db 63 DRCEYV 68

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RESULT 39
US-10-600-272-28
; Sequence 28, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-600-272-28

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Query Match          52.7%; Score 205; DB 16; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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Qy 3 ARITFGTWIYSVVK--EQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMEQHAKMY 60
Db 3 ARITFAMWRGRGLKQRPBELAENGFFYTGQDVKTRCCDGGGLKDWEPDAPWQHAKMY 62

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Qy 61 PGCKYL 66
Db 63 DRCEYV 68

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RESULT 40
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-041-859-12

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Query Match          52.7%; Score 205; DB 14; Length 172;
Best Local Similarity 50.0%; Pred. No. 1.5e-16;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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Qy 3 ARITFGTWIYSVVK--EQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMEQHAKMY 60

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Db	70	ARLRTFAWPRGLKORPELAEAGFFYTGOGBDKTRCFCCDGLKDWEPDAPWOOHAWY	129
Oy	61	PGCKYL	66
Db	130	DRCEYV	135

Search completed: June 15, 2005, 17:58:16
Job time : 108.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:19:12 ; Search time 112.5 Seconds
(without alignments)
300.420 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIFFTGWTIYSVNKEQ.....KPSDPWQHAKMYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	497	1	BIR4_HUMAN
2	377	96.9	496	1	BIR4_RAT
3	377	96.9	496	2	Q9E0F0
4	377	96.9	501	2	Q9E0D4
5	372	95.6	501	2	Q9E0D5
6	368	94.6	496	1	BIR4_MOUSE
7	347	89.2	236	1	BIR8_HUMAN
8	347	89.2	236	2	Q6PIA0
9	347	89.2	236	2	Q6IPY1
10	341	87.7	236	1	BIR8_PANTR
11	338	86.9	236	1	BIR8_GORGO
12	322	82.8	106	2	Q96RW6
13	287	73.8	493	2	Q8UVF8
14	255	65.6	109	2	Q8WNY4
15	219	56.3	280	2	Q6VTV9
16	216	55.5	322	2	Q6DBV7
17	216	55.5	405	2	Q8UWH2
18	216	55.5	415	2	Q7SX01
19	211	54.2	287	2	Q6E7G7
20	211	54.2	604	1	BIR3_HUMAN
21	209	53.7	358	1	PIAP_PIG
22	206	53.0	602	2	Q9E8E5
23	205	52.7	268	1	IAV3_NPVOP
24	204	52.4	195	2	Q9IA70
25	204	52.4	197	2	Q9IA69
26	204	52.4	611	1	BIR_CHICK
27	203	52.2	269	2	Q6OKJ6
28	203	52.2	374	2	Q921N0
29	203	52.2	600	1	BIR3_MOUSE
30	202	51.9	616	2	Q804E2
31	202	51.9	628	2	Q8UWD2

32	202	51.9	647	2	Q7T0K2
33	202	51.9	654	2	Q6ZM93
34	199	51.2	346	2	Q8IS31
35	199	51.2	346	2	Q968T8
36	198	50.9	589	2	Q9E8E8
37	198	50.9	589	2	Q9OZC6
38	197	50.6	534	2	Q8IZZ0
39	197	50.6	589	2	Q6P6S1
40	197	50.6	612	1	BIR2_MOUSE
41	197	50.6	618	1	BIR2_HUMAN
42	196	50.4	604	2	Q8OLK8
43	196	50.4	604	2	Q6DDY3
44	195	50.1	263	2	Q80SF4
45	195	50.1	403	2	Q8WRD9

ALIGNMENTS

RESULT 1
ID BIR4_HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9N014;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP-like protein) (HILP).
DE (IAP-like protein) (HILP).
GN Name=BIRC4; Synonyms=API3, IAP3, XIAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Tamblay C., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAI and a related family of IAP genes."
RL Nature 379:349-353(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Giffillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors."
RL EMBO J. 15:2685-2694(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC Grafiham D.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E., Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulvaney S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blaquesies R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmutz U.T., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.B., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]

RN FUNCTION.

RP MEDLINE=97373959; PubMed=9230442; DOI=10.1038/40901;

RA Devereaux O.L., Takahashi R., Salvesen G.S., Reed J.C.;"X-linked IAP is a direct inhibitor of cell-death proteases.";

RL Nature 388:300-304(1997). [6]

RN MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.

RX MEDLINE=21634829; PubMed=11604410; DOI=10.1074/jbc.M109891200;

RA Verhaeghe A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H., Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L., Simpson R.J., Vaux D.L.;"HcPro promotes cell death through its serine protease activity and ability to antagonize inhibitors of apoptosis proteins.";

RT J. Biol. Chem. 277:445-454(2002). [7]

RN STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.

RX MEDLINE=21020961; Pubmed=11140637; DOI=10.1038/35050006;

RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T., Herrmann J., Wu J.C., Fesik S.W.;"Structural basis for binding of Smac/DIABLO to the XIAP BIR3 domain".

RT Nature 408:1004-1008(2000).

-1- -FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.

-1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- TISSUE SPECIFICITY: Ubiquitous, except peripheral blood leukocytes.

-1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains.

-1- SIMILARITY: Belongs to the IAP family.

-1- SIMILARITY: Contains 3 BIR repeats.

-1- SIMILARITY: Contains 1 RING-type zinc finger.

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CC

EMBL; U45880; AAC50373.1; -.
EMBL; U32974; AAC50518.1; -.
DR EMBL; AL121601; CAB95312.1; -.
DR EMBL; BC032729; AAH32729.1; -.
PIR; S69544; S69544.
PDB; 1C9Q; NMR; A=124-240.
PDB; 1F9X; NMR; A=237-356.
PDB; 1G3F; NMR; A=240-356.
PDB; 1G73; X-ray; C/D=238-358.
PDB; 1I3O; X-ray; E/F=120-240.
PDB; 1I4Q; X-ray; E/F=120-260.
PDB; 1I51; X-ray; E/F=124-240.
PDB; 1KMC; X-ray; C/D=124-242.
PDB; 1NW9; X-ray; A=253-350.
GeneW; HGNC:592; BIRC4.
H-InVdB; HIX0017033; -.
MIM; 300079; -.
GO; GO:0005829; C:cytosol; TAS.
GO; GO:0043027; F:caspase inhibitor activity; IDA.
GO; GO:0006916; P:anti-apoptosis; TAS.
Interpro; IPRO01370; BIR.

DR	InterPro; IPR002097; Profilin.
DR	InterPro; IPR001841; Znf_ring.
DR	Pfam; PF00653; BIR; 3.
DR	SMART; SM00238; BIR; 3.
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.
DR	PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR	PROSITE; PSS00518; ZF_RING_1; FALSE_NEG.
KV	PROSITE; PSS00089; ZF_RING_2; 1.
KW	3D-structure; Apoptosis; Repeat; Thiol protease inhibitor; zinc-finger.
KW	REPEAT
FT	REPEAT 26 93
FT	BIR 1.
FT	BIR 2.
FT	BIR 3.
FT	RING-type.
FT	D->A: Reduced interaction with PRSS25;
FT	N->D: Reduced interaction with PRSS25;
FT	when associated with S-214.
FT	D->S: Reduced interaction with PRSS25;
FT	when associated with S-314.
FT	W->R: Reduced interaction with PRSS25;
FT	when associated with S-314.
FT	D->S: Reduced interaction with PRSS25.
FT	Reduced interaction with PRSS25; when associated with A-148.
FT	E->S: Decreased interaction with SMAC and with PRSS25. Decreases interaction with PRSS25; when associated with D-259 or A- 310.
FT	S -> C (1n Ref. 1).
FT	Q -> P (1n Ref. 2).
FT	CONFLICT 162 162
FT	CONFLICT 423 423

Seq	SEQUENCE	497 AA;	56684 MW;	9D394C16D45EB635 CRC64;
Query Match		100.0%;	Score 389;	DB 1;
Best Local Similarity		100.0%;	Pred. No. 7.5e-37;	
Matches	66;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 YEARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 60
 Db 265 YDARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 2

BIR4_RAT STANDARD; PRT; 496 AA.

AC Q9R016;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
 DE (IAP homolog A) (RIAP3) (RIAP-3).
 GN Name=Birc4; Synonyms=Ap13, XIap;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saito N.;
 RT "Rattus norvegicus X-linked inhibitor of apoptosis (xiap) mRNA."
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (by similarity).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC EMBL; AB033366; BAA85304.1; -.
 DR HSPSP, P98170; 1151.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SMO0238; BIR; 3.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Apoptosis; Repeat; Zinc-finger.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 264 329 BIR 3.
 FT ZN_FING 449 484 RING-type.
 SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 96.9%; Score 377; DB 1; Length 496;
 Best Local Similarity 95.5%; Pred. No. 1.9e-35;
 Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 60
 Db 264 YDARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 323
 QY 61 PGCKYL 66
 Db 324 PGCKYL 329

RESULT 3

Q9ESF0 PRELIMINARY; PRT; 496 AA.

AC Q9ESF0;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11860601;
 RA Holcik M., Jelebre C.A., Hicks K., Korneluk R.G.;
 RT "Cloning and characterization of the rat homologues of the inhibitor of Apoptosis protein 1, 2, and 3 genes."
 RL BMC Genomics 3:5-5(2002).
 DR EMBL; AF183429; AAG22969.1; -.
 DR HSPSP, P98170; 1151.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; P:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001370; Prot_inh_132_IAP.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SMO0238; BIR; 3.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAE5B798 CRC64;

Query Match 96.9%; Score 377; DB 2; Length 496;
 Best Local Similarity 95.5%; Pred. No. 1.9e-35;
 Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 60
 Db 264 YDARIPTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAKMY 323
 QY 61 PGCKYL 66
 Db 324 PGCKYL 329

RESULT 4

Q9EQ04 PRELIMINARY; PRT; 501 AA.

AC Q9EQ04;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Ovary;

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RX MEDLINE=22642584; PubMed=12606402;
RA Latreu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL; AF304334; AAC41193.1; -.
DR HSSP; P98170; 1151.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query Match 96.9%; Score 377; DB 2; Length 501;
Best Local Similarity 95.5%; Pred. No. 1.9e-35;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEQHAKWY 60
Db 264 YDARIIVTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEQHAKWY 323
QY 61 PGCKYTL 66
Db 324 PGCKYTL 329

RESULT 5
Q9E005 PRELIMINARY; PRT; 501 AA.
AC Q9E005;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RX MEDLINE=22642584; PubMed=12606402;
RA Latreu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL; AF304333; AAC41192.1; -.
DR HSSP; P98170; 1151.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56548 MW; 0973BF28B81C5A0 CRC64;

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Query Match 95.6%; Score 372; DB 2; Length 501;
Best Local Similarity 93.9%; Pred. No. 7.3e-35;
Matches 62; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEQHAKWY 60
Db 264 YDARIIVTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGLADWKPSDPMEQHAKWY 323
QY 61 PGCKYTL 66
Db 324 PGCKYTL 329

RESULT 6
BIR4 MOUSE
ID BIR4 MOUSE STANDARD; PRT; 496 AA.
AC Q60959; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN Name=Birc4; Synonyms=Aip4, Ap13, Miha, Xiap;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farhanli R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U68442; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSSP; P98170; 1151.
DR MGD; MGI:107572; Birc4.
DR GO; GO:0001719; P:inhibition of caspase activation; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.

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DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Repeat; Zinc-finger.
FT REPEAT 26
FT REPEAT 163
FT REPEAT 230
FT ZN_FING 264
FT ZN_FING 329
FT ZN_FING 449
FT ZN_FING 484
FT ZN_FING 208
FT ZN_FING 208
FT ZN_FING 317
FT ZN_FING 317
FT ZN_FING 322
FT ZN_FING 322
FT ZN_FING 346
FT ZN_FING 346
FT ZN_FING 360
FT ZN_FING 360
FT ZN_FING 388
FT ZN_FING 388
FT ZN_FING 449
FT ZN_FING 449
FT ZN_FING 462
FT ZN_FING 462
FT ZN_FING 468
FT ZN_FING 468
FT ZN_FING 490
FT ZN_FING 490
SQ SEQUENCE 496 AA; 56079 MW; ECSFAE0799F2CDD8 CRC64;

Query Match 94.6%; Score 368; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2.1e-34;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 60
DB 264 YEARIVFGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 7
BIR_HUMAN
ID BIR_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 05-JUL-2004 (Ref. 41, Last sequence update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=21481900; PubMed=11597143; DOI=10.1006/geno.2001.6635;
RA Legace M., Xuan J.-Y., Young S.S., McRoberts C., Maiter J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RA "Genomic organization of the X-linked inhibitor of apoptosis and
RA identification of a novel testis-specific transcript.";
RT Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=21286921; PubMed=11390657;
RA DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Elben L.J., Lewis J., Refey S.B.,
RA Praticelli A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Nottarangelo L.D., Vezoni P., Fearnhead H.O., Duckett C.S.;
RA "Molecular cloning of ILP-2, a novel member of the inhibitor of
RA apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX.
CC -1- SUBUNIT: Binds to caspase-9.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -1- SIMILARITY: Belongs to the IAP family.

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CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81992.1; -.
DR HSSP; P98170; 1G73.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; RING; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS01282; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger.
FT REPEAT 7
FT ZN_FING 189
FT ZN_FING 224
FT ZN_FING 196
FT ZN_FING 196
SQ SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;

Query Match 89.2%; Score 347; DB 1; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.0e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 60
DB 4 YEARIVFGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 8
O6PIAO
ID O6PIAO PRELIMINARY; PRT; 236 AA.
AC O6PIAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Baculoviral IAP repeat-containing 8.
GN Name=BIRC8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Slaton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC039318; AA039318.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 1.
DR SMART: SM00238; BIR; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 236 AA; 27077 MW; DP38350311PDAFPR CRC64;

Query Match 89.2%; Score 347; DB 2; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.8e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIITFGTWISVVKELARAGFYALGEGDKVCFHCGGGLTDMKPSDPEWQHAKMY 60
DB 4 YEARIITFGTWISVVKELARAGFYALGEGDKVCFHCGGGLANMKPRDEPWQHAKMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 9
Q6IPY1 PRELIMINARY; PRT; 338 AA.
ID Q6IPY1;
AC Q6IPY1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BIRC8 protein.
GN Name=BIRC8;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L., Shenmen C.M., Schlier G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hailton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC071665; AA071665.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 338 AA; 38622 MW; DC17979CF92E4DF CRC64;

Query Match 89.2%; Score 347; DB 2; Length 338;
Best Local Similarity 84.8%; Pred. No. 4.1e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIITFGTWISVVKELARAGFYALGEGDKVCFHCGGGLTDMKPSDPEWQHAKMY 60
DB 106 YEARIITFGTWISVVKELARAGFYALGEGDKVCFHCGGGLANMKPRDEPWQHAKMY 165
QY 61 PGCKYL 66
DB 166 PGCKYL 171

RESULT 10
BIR8_PANTR STANDARD; PRT; 236 AA.
ID BIR8_PANTR;
AC Q95W72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonyms=ILP2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1126/MB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Pratiini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DR Inhibitor of apoptosis protein 3.
GN Name=IAP3;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF451854; AL447170.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 73.8%; Score 287; DB 2; Length 493;
Best Local Similarity 71.2%; Pred. No. 6e-25;
Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEOHAKVY 60
DB 264 YERRIQFLAWIVYVNHLEHLAGFYSTGNDHYVCFHCGGGLQEMKENEDPMDOHAKMF 323
QY 61 PGCKYL 66
DB 324 PGCKFL 329

RESULT 14
Q8WMY4 PRELIMINARY; PRT; 109 AA.
ID Q8WMY4
AC Q8WMY4;
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN Name=XIAP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AL66179.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213D6ED CRC64;

Query Match 65.6%; Score 255; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 7.1e-22;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDWKP 48
DB 57 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDWKP 104

RESULT 15
Q6VTY9 PRELIMINARY; PRT; 280 AA.
ID Q6VTY9
AC Q6VTY9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
OS Inhibitor of apoptosis protein 3.
OC Choriostemonera fumiterana defective nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=74660;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138;
RA Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.;
RT "Characterization of an overexpressed spindle protein during a
RL baculovirus infection.";
RN Virology 268:56-67(2000).
[2]
RP SEQUENCE FROM N.A.
RA Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY327402; AA091688.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 280 AA; 32179 MW; CA8804614BFD1A1 CRC64;

Query Match 56.3%; Score 219; DB 2; Length 280;
Best Local Similarity 54.5%; Pred. No. 2.9e-17;
Matches 36; Conservative 13; Mismatches 15; Indels 2; Gaps 1;

QY 3 ARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEOHAKVY 60
DB 115 ARLKTFVDPVPSIKQRPQLAEGFYTGKGRVKCFHCDGGLKDWESTDEPWEHARWF 174
QY 61 PGCKYL 66
DB 175 DRCTYV 180

RESULT 16
Q6DBV7 PRELIMINARY; PRT; 322 AA.
ID Q6DBV7
AC Q6DBV7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL EMBL: BC078344; AAH78344.1; -;
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro: IPR001370; Prot_inh_132_IAP.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PSS0143; BIR_REPEAT_2; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 322 AA; 36412 MW; P9562546FA200CDF CRC64;
 Query Match 55.5%; Score 216; DB 2; Length 322;
 Best Local Similarity 53.0%; Pred. No. 7, 5e-17;
 Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMWQHAKWY 60
 DB 229 FEERLDSFKQRHPIPERLARAGFYSTGEQDRVWCFRCGGGVKAWMPDPMEEHARHY 288
 QY 61 PGCKYL 66
 DB 289 PGCSFL 294
 RESULT 17
 O8UWH2 PRELIMINARY; PRT; 405 AA.
 AC O8UWH2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Xlap.
 GN Name=birc4;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;

RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 RT zebrafish.";
 RL Cell Death Differ. 7:509-510(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: AF439767; AAJ32047.1; -;
 DR HSSP: P98170; 1130.
 DR ZFIN: ZDB-GENE-030625-7; birc4.
 DR GO: GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PSS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PSS0089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;
 Query Match 55.5%; Score 216; DB 2; Length 405;
 Best Local Similarity 53.0%; Pred. No. 9, 5e-17;
 Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMWQHAKWY 60
 DB 229 FEERLDSFKQRHPIPERLARAGFYSTGEQDRVWCFRCGGGVKAWMPDPMEEHARHY 288
 QY 61 PGCKYL 66
 DB 289 PGCSFL 294
 RESULT 18
 O7SKX1 PRELIMINARY; PRT; 415 AA.
 AC O7SKX1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Birc4 protein (Fragment).
 GN Name=birc4;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Straube R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BC055246; AAH55246.1; -.
DR HSPB; P98170; I130.
DR ZFIN; ZDB-GENE-030825-7; birc4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0089; ZF_RING_2; 1.
DR Metal-binding; zinc; Zinc-finger.
FT NON TER 1
SQ SEQUENCE 415 AA; 46788 MW; D9B82E448ADCA92 CRC64;

Query Match 55.5%; Score 216; DB 2; Length 415;
Best Local Similarity 53.0%; Pred. No. 9.7e-17;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIFFPTGWTIVSVNKEQALRAGAFYALGSGDKYKCFCHCGGGLTDMKPSDPMEQHAQWY 60
DB 240 PEGRLDSFKRGQHPIDPERLARACFYSTGEODVMCRGCGVYKAMPDEDDPMEHARHY 299
QY 61 PGCKYL 66
DB 300 PGCSFL 305

RESULT 19
Q6E7G7 PRELIMINARY; PRT; 287 AA.
AC Q6E7G7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE IAP-3.
OS Anticarsia gemmatilis nuclear polyhedrosis virus (AgMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=31507;
RN [1]
RP SEQUENCE FROM N.A.
RA Carpes M.P., Castro M.E., Soares E.F., Villela A.G., Pinedo F.J.,
RL Ribeiro B.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525121; AAS92269.1; -
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PSS01282; BIR_REPEAT_1; 2.
DR PROSITE; PSS0143; BIR_REPEAT_2; 2.
DR PROSITE; PSS0089; ZF_RING_2; 1.

SQ SEQUENCE 287 AA; 32620 MW; 20F3A7F0C11C4C2B CRC64;

Query Match 54.2%; Score 211; DB 2; Length 287;
Best Local Similarity 53.0%; Pred. No. 2.6e-16;
Matches 35; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY 3 ARIFPTGWTIVSVNKEQALRAGAFYALGSGDKYKCFCHCGGGLTDMKPSDPMEQHAQWY 60
DB 127 ARKTFEDWPLSLKORPEQLAEAGFYTGKDKYKCFCDGGLKDWANDEPMEHARWF 186
QY 61 PGCKYL 66
DB 187 DRCSFV 192

RESULT 20
BIR3_HUMAN STANDARD; PRT; 604 AA.
ID BIR3_HUMAN
AC Q13489; Q13489; Q9HC27; Q9UP46;
DT 01-NOV-1997 (Ref. 35, Created)
DT 01-NOV-1997 (Ref. 35, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 1) (IAP1) (H1AP1) (C-IAP2) (TNFR2-TRAF signaling complex protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (AIP2).
DE Name=BIR3; Synonyms=API2, IAP1, MICH;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,
RA Farahan R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by Nalp and a related
RT family of IAP genes.";
RL Nature 379:349-353 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes.";
RL Blood 93:3418-3431 (1999).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Klausner R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

RA Ditchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
 RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6].
 RP SEQUENCE OF 362-441 FROM N.A.
 RX MEDLINE=20519161; PubMed=11066071;
 RA DOI=10.1002/1098-2264(2000)999:999<:AID-GCCT1036>3.0.CO;2-I;
 RA Baens M., Steyls A., Diehlamm J., De Wolf-Peters C., Marynen P.,
 RT "Structure of the MALT gene and molecular characterization of the
 RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
 RT B-cell lymphomas of MALT type.";
 RL Genes Chromosomes Cancer 29:281-291 (2000).
 CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
 CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
 CC form an heteromeric complex, which is then recruited to the tumor
 CC necrosis factor receptor 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: Highly expressed in fetal lung, and kidney. In
 CC the adult, expression is mainly seen in lymphoid tissues.
 CC -1- Including spleen, thymus and peripheral blood lymphocytes.
 CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
 CC recurrent in low-grade MALT lymphoma (mucosa-associated lymphoid
 CC tissue). This translocation is found in approximately 50% of
 CC cytogenetically abnormal low-grade MALT lymphoma and involves
 CC MALT1 and BIRC3.
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW=http://www.infobiochem.fr/services/chromocancer/genes/BIRC3ID239.html".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
 CC or send an email to license@1sb-sib.ch).
 CC
 CC -----
 CC EMBL: LA9432; AAC41943.1; -;
 CC EMBL: U45878; AAC50371.1; -;
 CC EMBL: U37546; AAC50507.1; -;
 CC EMBL: AF070674; AAC83232.1; -;
 CC EMBL: BC037420; AAC37420.1; -;
 CC EMBL: AF178945; AAC09369.1; -;
 CC PIR: S68449; S68449.
 CC HSSP: Q13490; IOBH.
 CC Genew: HGNC:591; BIRC3.
 CC MIM: 601721.
 CC GO: GO:0005515; P:protein binding; NAS.
 CC GO: GO:0006916; P:cell apoptosis; TAS.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001315; CARD.
 CC InterPro: IPR011029; DEATH like.
 CC InterPro: IPR001841; Znf_fing.
 CC Pfam: Pf00653; BIR_3.

DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50143; CARD; 1.
 DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; zf_RING_2; 1.
 KW Apoptosis; Chromosomal translocation; Repeat; zinc-finger.
 FT REPEAT 29
 FT REPEAT 169
 FT REPEAT 255
 FT DOMAIN 439
 FT ZN FING 557
 FT SITE 442
 FT 443
 FT 18
 FT 119
 FT 153
 FT 163
 FT 165
 FT 191
 FT 191
 FT 364
 FT 552
 FT 552
 SQ SEQUENCE 604 AA; 68371 MW; 8581A0BA9AABA47 CRC64;
 Query Match 54.2%; Score 211; DB 1; Length 604;
 Best Local Similarity 57.4%; Pred. No. 5,4e-16;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
 QY 1 YEARIFPTGWITS--VNKEQLARAGFYALGEGDKVYCFHGGGLTPMKSPDPBEOHAK 58
 Db 255 HAARFPTFFWPSVVLNVEQLASAGFTYVGNSDVKFCDDGSLRCWESGDDEPVGHAK 314
 QY 59 WYPCCKYL 66
 Db 315 WPPRCETL 322
 RESULT 21
 RIAP PIG STANDARD; PRT; 358 AA.
 AC 062610;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative inhibitor of apoptosis.
 GN Name=RIAP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=98162622; PubMed=9501011; DOI=10.1006/birc.1998.8185;
 RA Stehlik C., de Martin R., Binder B.R., Lipp J.,
 RT "Cytokine induced expression of porcine inhibitor of apoptosis protein
 RT (Iap) family member is regulated by NF-kappa B.";
 RL Biochem. Biophys. Res. Commun. 243:827-832 (1998).
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 2 BIR repeats.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC
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CC -----

DR EMBL; L22564; AAC02610.1; -.
 DR EMBL; U75930; AAC59034.1; -.
 DR PIR; A53989; A53989.
 DR HSSP; Q24306; IUD4.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 2.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 2.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 2.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Apoptosis; Repeat; Zinc-finger.
 FT REPEAT 18 84 BIR 1.
 FT REPEAT 111 178 BIR 2.
 FT ZN FING 221 256 RING-type.
 SQ SEQUENCE 268 AA; 30076 MW; DF89175FDB85A708 CRC64;

Query Match 52.7%; Score 205; DB 1; Length 268;
 Best Local Similarity 50.0%; Pred. No. 1.2e-15;
 Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

QY 3 ARIFFTGWTWYVSVK--EQIARAGFYALGSDGKVKCFHCGGGLTDMKPSDDPMEQHAQX 60
 DB 113 ARIRTFMWRGRLKQRPBELAENGFYTGQGDKTRCCCGGLKDMWPDPAWQGHAKRY 172
 QY 61 PGCKYTL 66
 DB 173 DRCEYV 178

RESULT 24

Q91A70 PRELIMINARY; PRT; 195 AA.
 AC Q91A70;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Inhibitor of apoptosis 1 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=breed leghorn; TISSUE=Spleen;
 RX MEDLINE=21158006; PubMed=11261557;
 RA Zhou H., Liu W., Lamont S.J.;
 RT "Genetic variation among chicken lines and mammalian species in
 specific genes.";
 RT specific genes.";
 RL Poul. Sci. 80:284-288(2001).
 DR EMBL; AF221082; AAF35319.1; -.
 DR HSSP; Q13490; IOBH.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR001370; Prot_inh_132_IAP.
 DR Pfam; PF00653; BIR; 2.
 DR SMART; SM00238; BIR; 2.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 2.
 FT NON_TER 1 195
 FT NON_TER 195 195
 SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 52.4%; Score 204; DB 2; Length 195;
 Best Local Similarity 54.4%; Pred. No. 1.1e-15;
 Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFFTGWTW--IYSVNKEQLARAGFYALGSDGKVKCFHCGGGLTDMKPSDDPMEQHAQX 58
 DB 116 HEARVKTFTINWPRIPRIPIVQPEQLADAGFYVYGRNDVYKCFCCDGLRCWESGDDPWIEHAK 175
 QY 59 WYPGCKYL 66
 DB 176 WPRCEYL 183

RESULT 25

Q91A69 PRELIMINARY; PRT; 197 AA.
 AC Q91A69;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Inhibitor of apoptosis 1 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=breed Fayoumi; TISSUE=Spleen;
 RX MEDLINE=21158006; PubMed=11261557;
 RA Zhou H., Liu W., Lamont S.J.;
 RT "Genetic variation among chicken lines and mammalian species in
 specific genes.";
 RT specific genes.";
 RL Poul. Sci. 80:284-288(2001).
 DR EMBL; AF221083; AAF35320.1; -.
 DR HSSP; Q13490; IOBH.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR001370; Prot_inh_132_IAP.
 DR Pfam; PF00653; BIR; 2.
 DR SMART; SM00238; BIR; 2.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 2.
 FT NON_TER 1 197
 FT NON_TER 197 197
 SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF62351A CRC64;

Query Match 54.4%; Score 204; DB 2; Length 197;
 Best Local Similarity 54.4%; Pred. No. 1.2e-15;
 Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFFTGWTW--IYSVNKEQLARAGFYALGSDGKVKCFHCGGGLTDMKPSDDPMEQHAQX 58
 DB 117 HEARVKTFTINWPRIPRIPIVQPEQLADAGFYVYGRNDVYKCFCCDGLRCWESGDDPWIEHAK 176
 QY 59 WYPGCKYL 66
 DB 177 WPRCEYL 184

RESULT 26

BIR_CHICK STANDARD; PRT; 611 AA.
 AC Q90660; O57319;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
 protein).
 GN Name=ITA; Synonyms=IAP1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RA MEDLINE=97101112; PubMed=8945639;
RA Diaby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes.";
RL DNA Cell Biol. 15:981-988 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Embryonic fibroblast;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-1AP, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
RL Mol. Cell Biol. 17:7328-7341 (1997).
CC -1- FUNCTION: Apoptotic suppressor.
CC -1- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic according
CC to Ref. 2.
CC -1- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in
CC both cortical and medullary cells of the thymus. Expressed at
CC relatively high levels also in spleen, bursa, intestine and lung
CC and at very low levels in testis, brain and skeletal muscle.
CC -1- INDUCTION: High levels are induced within 4-8 hours of T-cell
CC activation in spleen and thymus.
CC -1- DOMAIN: The ring finger is important for its antiapoptotic effect.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
CC EMBL; U27466; AAB48118.1; "-
CC EMBL; AF008592; AAB88044.1; "-
CC HSSP; Q13490; IOBH.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR011029; DEATH_like.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS50143; BIR_REPEAT_2; 3.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS50018; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS50089; ZF_RING_2; 1.
CC KW Apoptosis; Nuclear protein; Repeat; Zinc-finger.
CC FT REPEAT 30 97
CC FT REPEAT 176 242 BIR 1.
CC FT REPEAT 262 329 BIR 2.
CC FT REPEAT 446 536 BIR 3.
CC FT ZN_FING 564 599 CARD.
CC FT CONFLICT 27 27 R -> L (in Ref. 2).
CC FT CONFLICT 150 150 R -> Q (in Ref. 2).
CC FT CONFLICT 169 169 Q -> H (in Ref. 2).
CC FT CONFLICT 183 183 S -> F (in Ref. 2).
CC FT CONFLICT 190 192 CLW -> PLS (in Ref. 2).
CC FT CONFLICT 196 196 V -> L (in Ref. 2).
CC FT CONFLICT 202 203 DD -> YY (in Ref. 2).
CC FT CONFLICT 213 214 VN -> FT (in Ref. 2).
CC FT CONFLICT 217 218 VK -> GQ (in Ref. 2).
CC FT CONFLICT 350 355 WNSRCT -> EQLS (in Ref. 2).
CC FT CONFLICT 359 359 K -> T (in Ref. 2).
CC FT CONFLICT 426 426 E -> D (in Ref. 2).
CC FT CONFLICT 492 492 T -> K (in Ref. 2).
CC FT CONFLICT 497 497 S -> L (in Ref. 2).
CC FT CONFLICT

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FT   COMPLETE 524 524 F -> C (in Ref. 2).
SQ   SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match
Best Local Similarity 52.4%; Score 204; DB 1; Length 611;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1.

QY 1 YEALITFGTWT--LYSVNKEQLAAGPVALGEGDKYKCFHCGGGLITDMPKSEDPWEQIAK 58
DB 262 HEAAVKEPIINPTRIPIVQPEQLAAGFYVGRNDVKFCFCCDGLRCWESGDDPWIEHAK 321
QY 59 WYPCCKYL 66
DB 322 WFPCEYL 329

RESULT 27
O6QXJ6 PRELIMINARY; PRT; 269 AA.
AC O6QXJ6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE ORF53.
GN Name=ORF53_IAP-1; ORFNames=AggVgP053;
OS Agrotis segetum granulosis virus (AgGV) (Agrotis segetum
OC Virusae; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
CX NCBI_Taxid=10464;
RN [1]
RP SEQUENCE FROM N.A.
RG Shanghai GeneCore Biotechnology Ltd;
RA Xitilian A., ZhiFang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
RA Yuhu S., Mei H.;
RT "Agrotis segetum Granulosis Virus complete genome.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RG Shanghai GeneCore Biotechnology Ltd;
RA Ai X.L., Wang Z.F., Wang B., Zhang W., Li F., Fu J.H., Cui C.S.,
RA Shi Y.H., He M.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RG Shanghai GeneCore Biotechnology Ltd;
RA Xitilian A., ZhiFang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
RA Yuhu S., Mei H.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY522332; AAS82685.1;
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znt_fing.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01283; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 269 AA; 31135 MW; C9296C534465EBC51 CRC64;

Query Match
Best Local Similarity 52.2%; Score 203; DB 2; Length 269;
Matches 33; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 2 EARLITFGTWTIYSV--NKEQLARAGFYALGEGDKYKCFHCGGGLITDMPKSEDPWEQIAK 59
DB 115 ENRLESTKTMVPVSIPLRPKELAAAGFYITGHSDQVNCFFYGGGGLRDKTGDDPWQIARW 174
QY 60 YPGCKYL 66
: : :

```

DB	175	PDKCFL 181
RESULT 28		
ID	0921NO	PRELIMINARY; PRT; 374 AA.
AC	0921NO	
DT	01-DEC-2001 (TREMBlrel. 19, Created)	
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)	
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)	
DE	Birc3 protein.	
GN	Name=Birc3; Synonyms=Birc2;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxId=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Czech II; TISSU= Mammary tumor;	
EX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;	
RA	Strausberg R., U., Uedon T.B., Yoshiyuki S., Carninci P., Schaefer C.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,	
RA	Alechl S.F., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,	
RA	Brownstein M.J., Uedon T.B., Yoshiyuki S., Carninci P., Schaefer C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Kryzhanek M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,	
RA	Jones S.J., Maira M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
Proc.	Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
LN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Czech II; TISSU= Mammary tumor;	
RA	Strausberg R.;	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC011338; AAI1338.1; -.	
DR	HSSP; Q13490; IOBH.	
DR	MGI; MGI:1197007; Birc3.	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0006916; P:anti-apoptosis; IEA.	
DR	Pfam; PF00653; BIR; 3.	
DR	SMART; SMO0238; BIR; 3.	
DR	PROSITE; PS01262; BIR_REPEAT_1; 3.	
DR	PROSITE; PS01443; BIR_REPEAT_2; 3.	
SO	SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7B46F3 CRC64;	
Query Match	52.2%; Score 203; DB 2; Length 374;	
Best Local Similarity	52.9%; Pred. No. 2,9e-15;	
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1		
QY	1 YEARIFTGWTWY--VNKEQIARAGFYALGEGDKYKCFHCGGGLTDMKPSDPEWEOHAK 58	
DB	253 HAARIRTSNWPSSALVHSGELASGFTYTGHSDDVKCFCCCGGRCWESGDDPWEVNAK 312	
QY	59 WYPGCKYL 66	
DB	313 WPPRCYEL 320	
RESULT 29		
ID	BIRC_MOUSE	STANDARD; PRT; 600 AA.
AC	BIRC_MOUSE	
OC	008863;	

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis
 DE protein 1) (MIAP) (MIAP-1).
 GN Name=Birc3; Synonyms=Birc2, Iap1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=Sketelal muscle;
 RA MEDLINE=96110590; PubMed=9441758; DOI=10.1006/geno.1997.5059;
 RX Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein
 RT 1 and 2 genes.";
 RL Genomics 46:495-503(1997).
 CC -!- FUNCTION: Apoptotic suppressor. The BIR motifs region interact
 CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
 CC form an heteromeric complex, which is then recruited to the tumor
 CC necrosis factor receptor 2 (TNFR2) (By similarity).
 CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
 CC inhibit apoptotic suppressor activity (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: Belongs to the IAP family.
 CC -!- SIMILARITY: Contains 3 BIR repeats.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----
 CC EMBL; U88908; AAC53531.1; -.
 CC HSSP; Q13490; IOBH.
 DR MGP; MGI:1197007; Birc2.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR010315; CARD.
 DR InterPro; IPR011029; DEATH_1like.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00097; Zf-C3HC4; 1.
 DR SMART; SMART0238; BIR; 3.
 DR SMART; SMO0184; CARD; 1.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS01263; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR Apoptosis; Repeat; zinc-finger.
 KW REPEAT; Repeat; zinc-finger.
 FT REPEAT 27
 FT REPEAT 167 233 BIR 1.
 FT REPEAT 253 320 BIR 2.
 FT DOMAIN 436 525 CARD.
 FT ZN_FING 553 588 RING-type.
 SQ SEQUENCE 600 AA; 67198 MW; AD7F73BE649317D1 CRC64;

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Db          313 WPRCEYL 320

RESULT 30
Q804E2      PRELIMINARY; PRT; 616 AA.
AC  Q804E2;
DT  01-JUN-2003 (TREMBlrel. 24, Created)
DT  01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Inhibitor of apoptosis protein-1.
GN  Name=CIAP-1;
OS  Ictalur punctatus (Channel catfish).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC  Ictaluridae; Ictalurus.
OX  NCBI_TaxId=7998;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Praveen K., Leary J.H. III, Evans D.L., Jaseo-Friedmann L.;
RL  Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR  EMBL: AY184377; AAC24632.1; -.
DR  HSSP: Q13490; 10BH.
DR  GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR  GO: GO:0005515; F:protein binding; IEA.
DR  GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR  GO: GO:0008270; F:zinc ion binding; IEA.
DR  GO: GO:0006916; P:anti-apoptosis; IEA.
DR  GO: GO:0016567; P:protein ubiquitination; IEA.
DR  GO: GO:0042981; P:regulation of apoptosis; IEA.
DR  InterPro: IPR011029; DEATH_1ike.
DR  InterPro: IPR001370; Prot_inh_132_IAP.
DR  InterPro: IPR001841; ZnF_Ring.
DR  Pfam: PF00653; BIR_3.
DR  Pfam: PF00619; CARD_1.
DR  SMART: SM00338; BIR_3.
DR  SMART: SM00114; CARD; 1.
DR  SMART: SM00184; RING; 1.
DR  PROSITE: PS01282; BIR_REPEAT_1; 2.
DR  PROSITE: PS50143; BIR_REPEAT_2; 3.
DR  PROSITE: PS50209; CARD; 1.
DR  PROSITE: PS50089; ZF_RING_2; 1.
KW  Metal-binding; zinc; zinc-finger.
SQ  SEQUENCE 616 AA; 69546 MW; D1389D915C6B256 CRC64;

Query Match          51.9%; Score 202; DB 2; Length 616;
Best Local Similarity 52.2%; Pred. No. 6.2e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY  2 EARLFTFGTW--LYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDTWKPSDEPMEQAAKY 59
DB  270 EERLLTFVMPARIPARPDOLAKAGFYVGRNDVXCFCCDGLRCWESGDDPWEVHAAY 329
QY  60 YPGCKYL 66
DB  330 FPRCEYL 336

RESULT 31
Q80WMD2     PRELIMINARY; PRT; 628 AA.
AC  Q80WMD2;
DT  01-MAR-2002 (TREMBlrel. 20, Created)
DT  01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Iap1.
GN  Name=birc3; Synonyms=iap1;
OS  Brachydanio rerio (Zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxId=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20373792; Pubmed=10917738;
RA  Inohara N., Nunez G.;
RT  "Genes with homology to mammalian apoptosis regulators identified in
RT  zebrafish.";
RL  Cell Death Differ. 7:509-510(2000).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Inohara N., Nunez G.;
RL  Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR  EMBL: AF442500; AAL33679.1; -.
DR  HSSP: Q13490; 10BH.
DR  ZFIN: ZDB-GENE-030825-6; birc3.
DR  GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR  GO: GO:0005515; F:protein binding; IEA.
DR  GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR  GO: GO:0008270; F:zinc ion binding; IEA.
DR  GO: GO:0006916; P:anti-apoptosis; IEA.
DR  GO: GO:0016567; P:protein ubiquitination; IEA.
DR  GO: GO:0042981; P:regulation of apoptosis; IEA.
DR  Pfam: PF00653; BIR_3.
DR  Pfam: PF00619; CARD; 1.
DR  Pfam: PF00097; ZF-C3HC4_1.
DR  SMART: SM00338; BIR_3.
DR  SMART: SM00114; CARD; 1.
DR  SMART: SM00184; RING; 1.
DR  PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR  PROSITE: PS50143; BIR_REPEAT_2; 3.
DR  PROSITE: PS50209; CARD; 1.
DR  PROSITE: PS50089; ZF_RING_2; 1.
KW  Metal-binding; zinc; zinc-finger.
SQ  SEQUENCE 628 AA; 70098 MW; 5B68CEBA87C8A95 CRC64;

Query Match          51.9%; Score 202; DB 2; Length 628;
Best Local Similarity 52.2%; Pred. No. 6.3e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY  2 EARLFTFGTW--LYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDTWKPSDEPMEQAAKY 59
DB  280 EERLLTFVMPSPRIPARPDOLAKAGFYVGRNDVXCFCCDGLRCWESGDDPWEVHAAY 339
QY  60 YPGCKYL 66
DB  340 FPRCEYL 346

RESULT 32
Q770K2     PRELIMINARY; PRT; 647 AA.
AC  Q770K2;
DT  01-OCT-2003 (TREMBlrel. 25, Created)
DT  01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Inhibitor of apoptosis protein.
GN  Name=birc3;
OS  Brachydanio rerio (Zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxId=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ens K.M., Valdimarsson G.;
RL  Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR  EMBL: AY247786; AAP04483.1; -.
DR  HSSP: P98170; 1130.
DR  ZFIN: ZDB-GENE-030825-6; birc3.
```

DR GO:00000151; C:ubiquitin ligase complex; IEA.
 DR GO:00005515; F:protein binding; IEA.
 DR GO:00004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO:00008270; F:zinc ion binding; IEA.
 DR GO:00006916; P:anti-apoptosis; IEA.
 DR GO:00016567; P:protein ubiquitination; IEA.
 DR GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR011029; DEATH_1like.
 DR InterPro: IPR001370; Prot_Inh_I32_IAP.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 647 AA; 72183 MW; 88DBBAFE92718FA9 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 647;
 Best Local Similarity 52.2%; Pred. No. 6.5e-15;
 Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARFTGTW--ITSVNEQLARAGFYALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAHW 59
 DB 299 EERLLTFVWNPSPRIPVAPDQAKAGFYVGRNDVCKFCGCCDGLRWESGDDPVWEHAKW 358
 QY 60 YPGCKYL 66
 DB 359 FPRCEYL 365

RESULT 33
 Q6ZM93 PRELIMINARY; PRT; 654 AA.

AC Q6ZM93 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE S1:B2P1.6.2 (Baculoviral IAP repeat-containing 3).
 GN Name1rc3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark G.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: AL627325; CAB47763.1; -;
 DR GO:00000151; C:ubiquitin ligase complex; IEA.
 DR GO:00005515; F:protein binding; IEA.
 DR GO:00004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO:00008270; F:zinc ion binding; IEA.
 DR GO:00006916; P:anti-apoptosis; IEA.
 DR GO:00016567; P:protein ubiquitination; IEA.
 DR GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR011029; DEATH_1like.
 DR InterPro: IPR001370; Prot_Inh_I32_IAP.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 654 AA; 72995 MW; A12425DE41A0259 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 654;
 Best Local Similarity 52.2%; Pred. No. 6.6e-15;
 Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARFTGTW--ITSVNEQLARAGFYALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAHW 59
 DB 306 EERLLTFVWNPSPRIPVAPDQAKAGFYVGRNDVCKFCGCCDGLRWESGDDPVWEHAKW 365
 QY 60 YPGCKYL 66
 DB 366 FPRCEYL 372

RESULT 34
 Q8IS31 PRELIMINARY; PRT; 346 AA.

AC Q8IS31 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Inhibitor of apoptosis protein.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Lepidoptera; Arthropoda; Glossata; Ditytalia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OC NCBI_TaxId=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang G., Wang L., Wu X.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY155274; AAN46650.1; -;
 DR HSSP: Q24306; 1040.
 DR GO:00000151; C:ubiquitin ligase complex; IEA.
 DR GO:00004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO:00008270; F:zinc ion binding; IEA.
 DR GO:00006916; P:anti-apoptosis; IEA.
 DR GO:00016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001370; Prot_Inh_I32_IAP.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00653; BIR; 2.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 2.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 346 AA; 36849 MW; 5450EB75F56A8486 CRC64;

Query Match 51.2%; Score 199; DB 2; Length 346;
 Best Local Similarity 50.0%; Pred. No. 7.8e-15;
 Matches 33; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIETFTWISVNE--EQIARAGFYALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAHW 60
 DB 184 ARIATFDWPRCKRQKREIELAAGFYVGGDKTKCFYCDGGLKWDSDVWPWEHARWF 243
 QY 61 PGCKYL 66
 DB 244 DRCAVY 249

RESULT 35
 Q968T8 PRELIMINARY; PRT; 346 AA.
 AC Q968T8 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Created)

```
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Archipoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
ON NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240184; PubMed=11341966; DOI=10.1016/S0167-4889(00)00105-1;
RA Huang Q., Devereux Q.L., Maeda S., Stenicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) from Bombyx mori.";
RL Biochim. Biophys. Acta 1499:191-198(2001).
DR EMBL; AF281073; AAKS7560.1; -.
DR HSPB; Q24306; I04Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CF6C6468894C69 CRC64;

Query Match 51.2%; Score 199; DB 2; Length 346;
Best Local Similarity 50.0%; Pred. No. 7.8e-15;
Matches 33; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIFFTGWTIVSVNK--EQIARAGFYALGEGDKVCKFCGGGLTDMKPSDPMEOHAKWY 60
DB 184 ARATFMDVPRBMRKQPEBELAAGFFYTCGCDKCKFCYCGGLDWDMSDDVPMQGHARWF 243
QY 61 PGCKYKL 66
DB 244 DRCAVY 249

RESULT 36
Q9SEB8 PRELIMINARY; PRT; 589 AA.
AC Q9SEB8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes.";
RL BMC Genomics 3:5-5(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF183431; AAG22971.1; -.
DR HSPB; Q13490; I0BH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
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DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_1like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 50.9%; Score 198; DB 2; Length 589;
Best Local Similarity 52.9%; Pred. No. 1.7e-14;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTGWTIVS--VNKEQLARAGFYALGEGDKVCKFCGGGLTDMKPSDPMEOHAK 58
DB 241 HSARMTFLVWPSVAVQPEQLASAGFYVDNDVCKFCDCGLRCWBERGDDPMIEHAK 300
QY 59 WYPCCKYL 66
DB 301 WPRCEPL 308

RESULT 37
Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22020585; PubMed=12023884; DOI=10.1042/BJ20011431;
RA Dong Z., Nishiyama J., Yi X., Venkatchalam M.A., Denton M., Gu S.,
RA Li S., Qiang M.;
RT "Gene promoter of apoptosis inhibitory protein IAP2: identification of
RT enhancer elements and activation by severe hypoxia.";
RL Biochem. J. 364:413-421(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF190020; AAF04585.1; -.
DR HSPB; Q13490; I0BH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_1like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
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Db      301 WPCRCEPL 308

RESULT 40
BIR2_MOUSE STANDARD; PRT; 612 AA.
ID_BIR2_MOUSE
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUN-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
protein 2) (MIAF2) (MIAF-2).
GN Name=Birc2; Synonyms=Birc3, Iap2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel P.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252 (1995).
[2]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758; DOI=10.1006/geno.1997.5059;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503 (1997).
CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form a heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; LA9433; AAC42078.1; -.
DR EMBL; U88909; AAC53532.1; -.
DR HSSP; Q13490; IQBH.
DR MGD; MGI:1197009; Birc3.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.

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DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Direct protein sequencing; Repeat; Zinc-finger.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-type.
FT CONFLICT 380 380 E -> K (in Ref. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 612;
Best Local Similarity 52.9%; Pred. No. 2,4e-14;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFPGWIVS--VNKEQLARAGFYALGEGDKYKCFHGGGGLTDWKPSDDPWGQHAH 58
DB 262 HSA RLRTFLYPPSPVQPEQLASAGFTYVDRNDVKCFCCDGLKCMERGGDPPWLEHAK 321
QY 59 WYPGCKYL 66
DB 322 WPCRCEPL 329

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Search completed: June 15, 2005, 17:39:36
 Job time : 113.5 secs